

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:47:08 ; Search time 18.4646 seconds
(without alignments)

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Title: US-10-774-076-14
Perfect score: 561
Sequence: 1 DIQMTQSPSSLISASVGVDRVT.....CLOYDPEPPYTFGGGTRVEIK 107

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/podata/1/1aa/5A_COMBO.pep:**
2: /cgn2_6/podata/1/1aa/5B_COMBO.pep:**
3: /cgn2_6/podata/1/1aa/6A_COMBO.pep:**
4: /cgn2_6/podata/1/1aa/6B_COMBO.pep:**
5: /cgn2_6/podata/1/1aa/PCTUS_COMBO.pep:**
6: /cgn2_6/podata/1/1aa/backfiled1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	510	90.9	107 2	US-08-290-592B-20 Sequence 20, Appl 17, App
2	510	90.9	107 5	PCT-US96-0948-20 Sequence 20, Appl 17, App
3	510	90.9	107 1	US-08-107-669D-27 Sequence 27, Appl 27, App
4	502	89.5	107 1	US-08-477-788A-125 Sequence 27, Appl 27, App
5	502	89.5	107 2	US-08-77-531B-27 Sequence 27, Appl 27, App
6	502	89.5	107 2	US-08-082-842A-27 Sequence 27, Appl 27, App
7	499	88.9	107 4	US-03-647-468-107 Sequence 27, Appl 27, App
8	499	88.9	127 4	US-09-647-468-182 Sequence 182, App
9	498	88.8	107 1	US-08-425-336-125 Sequence 125, App
10	498	88.8	107 1	US-08-488-113B-148 Sequence 125, App
11	498	88.8	107 1	US-08-488-113B-125 Sequence 125, App
12	498	88.8	107 1	US-08-477-484B-125 Sequence 125, App
13	498	88.8	107 1	US-08-107-669D-65 Sequence 125, App
14	498	88.8	107 1	US-03-472-788A-87 Sequence 107, Appl
15	498	88.8	107 2	US-08-477-531B-65 Sequence 65, Appl
16	498	88.8	107 2	US-08-646-360-125 Sequence 125, App
17	498	88.8	107 2	US-08-842A-87 Sequence 87, Appl
18	498	88.8	107 3	US-08-839-765-125 Sequence 125, App
19	498	88.8	107 3	US-03-136-3389-125 Sequence 125, App
20	498	88.8	107 3	US-03-610-838-125 Sequence 125, App
21	498	88.8	107 4	US-03-711-485-125 Sequence 125, App
22	495	88.2	240 1	US-08-488-113B-147 Sequence 147, App
23	495	88.2	240 1	US-08-488-113B-148 Sequence 147, App
24	495	88.2	240 1	US-08-477-484B-147 Sequence 147, App
25	495	88.2	240 1	US-08-477-484B-148 Sequence 147, App
26	495	88.2	240 2	US-08-646-3360-148 Sequence 148, App
27	88.2			

RESULT 1
US-08-290-592B-20
; Sequence 20, Application US/08290592B
; Patent No. 5824307
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, L.
; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
; TITLE OF INVENTION: Respiratory Syncytial Virus
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &
; ATTORNEY/AGENT INFORMATION:
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,592B
; FILING DATE: August 15, 1994
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/813,372
; FILING DATE: December 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ostein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 469201-257
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN

US-08-290-592B-20
Query Match Score 510; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 42e-44;
Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLISASVGVDRVTCKASDINNSVLSWFOOKPGKPKTLYRANRLVDPVS 60

Db

1 DIQMTQSITLSAVGRVITCKASODINRYLNWYQQKGAKPLIYRANRLVDGVPS 60

Qy

61 RFSGSGSGQDTISLQPEDATPYCQYDERPYTPGGTKVEIK 107

Dd

61 RFSGSGSGTEFLITISLQPDATPYCQYDERPYTPGGTKVEIK 107

RESULT 2

PCT-US95-10053-17

; Sequence 17, Application PC/TUS9510053

; GENERAL INFORMATION:

; APPLICANT: JOHNSON, L.

; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against Respiratory Syncytial

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESS: CECCHI, STUART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/09448

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/290,592

; FILING DATE: August 15, 1994

; APPLICATION NUMBER: 07/813,372

; CURRENT APPLICATION DATA:

; FILING DATE: December 23, 1991

; CLASSIFICATION: Concurrently

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/290,592

; FILING DATE: August 15, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/813,372

; CURRENT APPLICATION DATA:

; FILING DATE: December 23, 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 449201-274

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 107 AMINO ACIDS

; TYPE: AMINO ACID

; STRANDEDNESS:

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN

; PCT-US95-10053-17

; Query Match 90.9%; Score 510; DB 5; Length 107;

; Best Local Similarity 88.8%; Pred. No. 4.2e-44; Mismatches 95; Conservative 8; Indels 0; Gaps 0; Matches 95; Mismatches 4;

; Qy 1 DIQMTQSITLSAVGRVITCKASODINRYLNWYQQKGAKPLIYRANRLVDGVPS 60

; Db 1 DIQMTQSITLSAVGRVITCKASODINRYLNWYQQKGAKPLIYRANRLVDGVPS 60

; Qy 61 RFSGSGSGQDTISLQPEDATPYCQYDERPYTPGGTKVEIK 107

; Db 61 RFSGSGSGTEFLITISLQPDATPYCQYDERPYTPGGTKVEIK 107

; RESULT 3

; PCT-US96-09448-20

; sequence 20, Application PC/TUS9609448

; GENERAL INFORMATION:

; APPLICANT: JOHNSON, L.

; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against Respiratory Syncytial

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESS: CECCHI, STUART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/107,669D

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/290,592

; FILING DATE: August 15, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: HERRON, CHARLES J.

; REGISTRATION NUMBER: 28,019

; REFERENCE/DOCKET NUMBER: 463201-257

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; FILING DATE: December 23, 1991

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 107 AMINO ACIDS

; TYPE: AMINO ACID

; STRANDEDNESS:

; TOPOLOGY: LINEAR

; PCT-US96-09448-20

; Query Match 90.9%; Score 510; DB 5; Length 107;

; Best Local Similarity 88.8%; Pred. No. 4.2e-44; Mismatches 95; Conservative 8; Indels 0; Gaps 0; Matches 95; Mismatches 4;

; Qy 1 DIQMTQSITLSAVGRVITCKASODINRYLNWYQQKGAKPLIYRANRLVDGVPS 60

; Db 1 DIQMTQSITLSAVGRVITCKASODINRYLNWYQQKGAKPLIYRANRLVDGVPS 60

; Qy 61 RFSGSGSGQDTISLQPEDATPYCQYDERPYTPGGTKVEIK 107

; Db 61 RFSGSGSGTEFLITISLQPDATPYCQYDERPYTPGGTKVEIK 107

; RESULT 4

; US-08-107-669D-27

; Sequence 27, Application US/08/107669D

; Patent No. 576686

; GENERAL INFORMATION:

; APPLICANT: Studnicka, Gary M.

; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)

; NUMBER OF SEQUENCES: 67

; CORRESPONDENCE ADDRESS:

; ADDRESS: Sternke, Kessler, Goldstein and Fox P.L.L.C.

; STREET: 1100 New York Ave., N.W., Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: United States of America

; ZIP: 20004-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/107,669D

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/290,592

; FILING DATE: August 15, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: HERRON, CHARLES J.

; REGISTRATION NUMBER: 28,019

; REFERENCE/DOCKET NUMBER: 463201-257

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; FILING DATE: December 23, 1991

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 107 AMINO ACIDS

; TYPE: AMINO ACID

; STRANDEDNESS:

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN

; PCT-US96-09448-20

FILED DATE: 13-AUG-1993
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/10906
 FILING DATE: 14-DEC-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/808,464
 FILING DATE: 13-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Michele A. Cimbala
 REGISTRATION NUMBER: 33,851
 REFERENCE/DOCKET NUMBER: 0610.1000001/MAC

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202/371-2600
 TELEFAX: 202/371-2540
 TELEX:

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-477-669B-27

Query Match 89.5%; Score 502; DB 1; Length 107;
 Best Local Similarity 88.8%; Pred. No. 2.6e-43; Mismatches 6; Indels 0; Gaps 0;
 Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIOMTOSPPSISASVGDRVTICKASQDINSYLSWFOQKRGKAPKLIVANRLVGDYPS 60
 Db 1 DIOMTOSPPSISASVGDRVTICKASQDINSYLSWFOQKRGKAPKLIVANRLVGDYPS 60

Qy 61 RFSSGSGSQYDTLISLOPEDFATYCQYDDEFRTFGGTKEIK 107
 Db 61 RFSSGSGSQYDTLISLOPEDFATYCQYDDEFRTFGGTKEIK 107

Qy 61 RFSSGSGSQYDTLISLOPEDFATYCQYDDEFRTFGGTKEIK 107
 Db 61 RFSSGSGSQYDTLISLOPEDFATYCQYDDEFRTFGGTKEIK 107

RESULT 5
 US-08-472-788A-27
 Sequence 27, Application US/08472788A
 Patent No. 577036
 Db 1 DIOMTOSPPSISASVGDRVTICKASQDINSYLSWFOQKRGKAPKLIVANRLVGDYPS 60

GENERAL INFORMATION:
 APPLICANT: Studnicka, Gary M.
 TITLE OF INVENTION: Modified Antibody Variable Domains
 NUMBER OF SEQUENCES: 89
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
 STREET: 1100 New York Ave., N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3934

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,531B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 436
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/107,669
 FILING DATE: 13-AUG-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/10906
 FILING DATE: 14-DEC-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/808,464
 FILING DATE: 13-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Michele A. Cimbala
 REGISTRATION NUMBER: 33,851
 REFERENCE/DOCKET NUMBER: 0610.1000004/MAC

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202/371-2600
 TELEFAX: 202/371-2540
 TELEX:

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-477-531B-27

Query Match 89.5%; Score 502; DB 1; Length 107;
 Best Local Similarity 88.8%; Pred. No. 2.6e-43; Mismatches 6; Indels 0; Gaps 0;
 Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIOMTOSPPSISASVGDRVTICKASQDINSYLSWFOQKRGKAPKLIVANRLVGDYPS 60
 Db 1 DIOMTOSPPSISASVGDRVTICKASQDINSYLSWFOQKRGKAPKLIVANRLVGDYPS 60

Qy 61 RFSSGSGSQYDTLISLOPEDFATYCQYDDEFRTFGGTKEIK 107
 Db 61 RFSSGSGSQYDTLISLOPEDFATYCQYDDEFRTFGGTKEIK 107

RESULT 6
 US-08-477-531B-27
 Sequence 27, Application US/08477531B
 Patent No. 5821123
 GENERAL INFORMATION:
 APPLICANT: Studnicka, Gary M.
 TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
 NUMBER OF SEQUENCES: 67
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
 STREET: 1100 New York Ave., N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: United States of America
 ZIP: 20005-3934

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,531B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 436
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/107,669
 FILING DATE: 13-AUG-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/10906
 FILING DATE: 14-DEC-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/808,464
 FILING DATE: 13-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Michele A. Cimbala
 REGISTRATION NUMBER: 33,851
 REFERENCE/DOCKET NUMBER: 0610.1000004/MAC

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202/371-2600
 TELEFAX: 202/371-2540
 TELEX:

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-477-531B-27

Query Match Best Local Similarity 89.5%; Score 522; DB 2; Length 107; Matches 95; Conservative 88.8%; Pred. No. 2.6e-43; 6; Mismatches 6; Indels 0; Gaps 0;

RESULT 7 US-08-082-842A-27 Sequence 27, Application US/08082842A

Patent No. 5859619

GENERAL INFORMATION:

APPLICANT: Studnicke, Gary M.

TITLE OF INVENTION: Modified Antibody Variable Domains

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:

ADDRESSEE: Steerne, Kessler, Goldstein and Fox P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: D.C.

country: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/082,842A

FILING DATE: 23-JUN-1993

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: -PCT/US92/10906

FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:

FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Cimbara, Michele A.

REGISTRATION NUMBER: 33, 851

REFERENCE/DOCKET NUMBER: 0610.100002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/371-2600

TELEX: 202/371-2540

TELEFAX: 202/371-2540

TELEX:

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

08-082-842A-27

Query Match Best Local Similarity 89.5%; Score 502; DB 2; Length 107; Matches 95; Conservative 88.8%; Pred. No. 2.6e-43; 6; Mismatches 6; Indels 0; Gaps 0;

RESULT 8 US-08-082-842A-27 Sequence 27, Application US/08082842A

Patent No. 5859619

GENERAL INFORMATION:

APPLICANT: SATO, KOH

APPLICANT: ADACHI, HIDEKI

APPLICANT: YABUTA, NAOIRO

TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND FILE REFERENCE: 053465/023

CURRENT APPLICATION NUMBER: US/08/082,842A

CURRENT FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: PCT/JP99/01768

PRIOR FILING DATE: 1999-04-02

PRIOR APPLICATION NUMBER: JPN 10-91850

PRIOR FILING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 183

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO: 107

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence coding of version "b1" of humanized L

OTHER INFORMATION: sequence coding of version "b1" of humanized L

OTHER INFORMATION: chain V region

US-09-647-468-107

Query Match Best Local Similarity 88.9%; Score 499; DB 4; Length 107; Matches 96; Conservative 87.7%; Pred. No. 5.3e-43; 3; Mismatches 8; Indels 0; Gaps 0;

RESULT 9 US-09-647-468-107 Sequence 107, Application US/09647468

Patent No. 6677436

GENERAL INFORMATION:

APPLICANT: SATO, KOH

APPLICANT: ADACHI, HIDEKI

APPLICANT: YABUTA, NAOIRO

TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND FILE REFERENCE: 053466/0289

CURRENT APPLICATION NUMBER: US/09/647,468

CURRENT FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: PCT/JP99/01768

PRIOR FILING DATE: 1999-04-02

PRIOR APPLICATION NUMBER: JP 10-91850

PRIOR FILING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 183

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO: 182

LENGTH: 127

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence coding of version "b1" of humanized L

OTHER INFORMATION: sequence coding of version "b1" of humanized L

OTHER INFORMATION: chain V region

US-09-647-468-182

Query Match Best Local Similarity 88.9%; Score 499; DB 4; Length 107; Matches 96; Conservative 87.7%; Pred. No. 5.3e-43; 3; Mismatches 8; Indels 0; Gaps 0;

RESULT 10 US-09-647-468-107 Sequence 107, Application US/09647468

Patent No. 6677436

GENERAL INFORMATION:

APPLICANT: SATO, KOH

APPLICANT: ADACHI, HIDEKI

APPLICANT: YABUTA, NAOIRO

TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND FILE REFERENCE: 053466/0289

CURRENT APPLICATION NUMBER: US/09/647,468

CURRENT FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: PCT/JP99/01768

PRIOR FILING DATE: 1999-04-02

PRIOR APPLICATION NUMBER: JP 10-91850

PRIOR FILING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 183

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO: 182

LENGTH: 127

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence coding of version "b1" of humanized L

OTHER INFORMATION: sequence coding of version "b1" of humanized L

OTHER INFORMATION: chain V region

US-09-647-468-182

QY 1 DIQMTQSPSISASVGDRVTICKASQDINSVLSWFOQKGKAPTKLIVRANLVDGVPS 60
 Db 21 DIQMTQSPSISASVGDRVTICKASQDINSVLSWFOQKGKAPTKLIVRANLVDGVPS 80
 Qy 61 RFSGGSGQDTLTSLOPEDFATYCYCLOQDEPFYFGGTKVIK 107
 Db 81 RFSGGSGQDTLTSLOPEDFATYCYCLOQDEPFYFGGTKVIK 127

RESULT 10
 US-08-425-336-125
 Sequence 125, Application US/08425336
 Patent No. 5621083
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnica, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606-6402

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/425, 336
 FILING DATE: 18-APR-1995
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/064, 691
 FILING DATE: 12-MAY-1993
 APPLICATION NUMBER: US 07/901, 707
 FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/064, 691
 FILING DATE: 12-MAY-1993
 APPLICATION NUMBER: US 07/901, 707
 FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988, 430
 FILING DATE: 09-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/488, 113B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/425, 336
 FILING DATE: 18-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064, 691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988, 430
 FILING DATE: 09-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Meyers, Thomas C.
 REGISTRATION NUMBER: P-36, 989
 REFERENCE/DOCKET NUMBER: 31394
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 125:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-425-336-125

Query Match 88.8%; Score 498; DB 1; Length 107;
 Best Local Similarity 89.7%; Pred. No. 6.7e-43; Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSISASVGDRVTICKASQDINSVLSWFOQKGKAPTKLIVRANLVDGVPS 60
 Db 1 DIQMTQSPSISASVGDRVTICKASQDINSVLSWFOQKGKAPTKLIVRANLVDGVPS 60
 Qy 61 RFSGGSGQDTLTSLOPEDFATYCYCLOQDEPFYFGGTKVIK 107
 Db 61 RFSGGSGQDTLTSLOPEDFATYCYCLOQDEPFYFGGTKVIK 107
 61 RFSGGSGQDTLTSLOPEDFATYCYCLOQDEPFYFGGTKVIK 107

RESULT 11
 US-08-488-113B-125
 Sequence 125, Application US/08488113B
 Patent No. 5744580
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnica, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 NUMBER OF SEQUENCES: 169
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOSS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/488, 113B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/425, 336
 FILING DATE: 18-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064, 691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988, 430
 FILING DATE: 09-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 125:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-488-113B-125

Query Match 88.8%; Score 498; DB 1; Length 107;
 Best Local Similarity 89.7%; Pred. No. 6.7e-43; Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSISASVGDRVTICKASQDINSVLSWFOQKGKAPTKLIVRANLVDGVPS 60
 Db 1 DIQMTQSPSISASVGDRVTICKASQDINSVLSWFOQKGKAPTKLIVRANLVDGVPS 60
 Qy 61 RFSGGSGQDTLTSLOPEDFATYCYCLOQDEPFYFGGTKVIK 107
 Db 61 RFSGGSGQDTLTSLOPEDFATYCYCLOQDEPFYFGGTKVIK 107

RESULT 12

US-08-477-484B-125

; Sequence 125, Application US/08477484B

; Patent No. 5716699

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnicka, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; NUMBER OF INVENTION: Proteins

; NUMBER OF SEQUENCES: 169

; CORRESPONDENCE ADDRESS:

; ADDRESSE: McAndrews, Held & Malloy, Ltd.

; STREET: 500 West Madison Street, 34th floor

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60661

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/477,484B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/425,336

; FILING DATE: 18-APR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/064,691

; FILING DATE: 12-MAY-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/988,430

; FILING DATE: 09-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/901,707

; FILING DATE: 19-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/787,567

; FILING DATE: 04-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Menicholas, Janet M.

; REGISTRATION NUMBER: 31,918

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/707-8839

; TELEFAX: 312/707-9155

; TELEX: 650 388-1248

; INFORMATION FOR SEQ ID NO: 125:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 107 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-477-484B-125

RESULT 13

US-08-107-669D-65

; Sequence 65, Application US/081.07669D

; Patent No. 5716886

; GENERAL INFORMATION:

; APPLICANT: Studnicka, Gary M.

; TITLE OF INVENTION: Modified Antibody Variable Domains

; NUMBER OF SEQUENCES: 89

; CORRESPONDENCE ADDRESS:

; ADDRESSE: Stern, Kessler, Goldstein and Fox P.L.L.C.

; STREET: 1100 New York Ave., N.W., Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3934

RESULT 14

US-08-472-788A-87

; Sequence 87, Application US/08472788A

; Patent No. 5770196

; GENERAL INFORMATION:

; APPLICANT: Studnicka, Gary M.

; TITLE OF INVENTION: Modified Antibody Variable Domains

; NUMBER OF SEQUENCES: 89

; CORRESPONDENCE ADDRESS:

; ADDRESSE: Stern, Kessler, Goldstein and Fox P.L.L.C.

; STREET: 1100 New York Ave., N.W., Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3934

Query Match Best Local Similarity 89.8%; Score 498; DB 1; Length 107; Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSVSWFOOKPGKAPTKIYRANLVDGVS 60
Db 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSVSWFOOKPGKAPTKIYRANLVDGVS 60

Qy 61 RPSGGSGGSDGYLTTSIQQPDEFAVYCLQWPFYPRGGTKEIK 107
Db 61 RPSGGSGGSDGYLTTSIQQPDEFAVYCLQWPFYPRGGTKEIK 107

RESULT 14
US-08-472-788A-87
Sequence 87, Application US/08472788A
Patent No. 5770196
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSE: Stern, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,788A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/082,842

FILING DATE: 22-JUN-1993

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10906

FILING DATE: 14-DEC-1992

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/808,464

FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Michele A. Cimbalia

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 0610.1000004/MAC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/371-2600

TELEFAX: 202/371-2540

INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

TOPology: linear

MOLECULE TYPE: protein

Query Match 88.8%; Score 498; DB 1; Length 107;
 Best Local Similarity 89.7%; Pred. No. 6.7e-43; Indels 0; Gaps 0;
 Matches 96; Conservative 3; Mismatches 8;

Qy 1 DIQMOSPSLSSASVGDRVITCKASQDINSYLSWFQKRGKAKPTLYRANLVDGVS 60
 Db 1 DIQMOSPSLSSASVGDRVITCRASQDINSYLSWFQKRGKAKPTLYRANLLESGVs 60

Qy 61 RFSGSGSGQDYLTISIQPEDPATYCYCLODEPYTFCGGTKWEIK 107
 Db 61 RFSGSGSGQDYLTISIQPEDPATYCYCLODEPYTFCGGTKWEIK 107
 61 RFSGSGSGQDYLTISIQPEDFGIYCCQYDBSPWTFGGTKWEIK 107

Search completed: December 29, 2004, 18:09:14
 Job time : 19.4646 Secs

RESULT 15

US 08-477-531B-65

Sequence 65 Application US/08477531B

Patent No. 5821123

GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.

TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.COUNTRY: United States of America
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,531B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 436

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/107,669

THIS
IS A
BLANK (USP).

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model
Run on: December 29, 2004, 17:47:08 ; Search time 20.5354 Seconds
384.304 Million cell updates/sec

Title: US-10-774-076-2
Perfect score: 648
Sequence: 1 BIQLOQSGPVELVKPGASVKV.....GNFPYTFDYMGSQGTTLTVSS 119
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 476139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/pctdata/1/iaa/5a_COMB.pep:*

2: /cgn2_6/pctdata/1/iaa/5b_COMB.pep:*

3: /cgn2_6/pctdata/1/iaa/6a_COMB.pep:*

4: /cgn2_6/pctdata/1/iaa/6b_COMB.pep:*

5: /cgn2_6/pctdata/1/iaa/pcmts_COMB.pep:*

6: /cgn2_6/pctdata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result	No.	Score	Query	Match Length	DB ID	Description
1	560..5	86.5	118 4	US-09-647-468-139	Sequence 139, APP	RESULT 1 US-09-647-468-139 ; Sequence 139, Application US/09647468 ; Patent No. 6677436 ; GENERAL INFORMATION: ; APPLICANT: SATO, KOH ; ATTORNEY: ADACHI, HIDEKI ; APPLICANT: YABUTA, NAOHIRO ; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY ; FILE REFERENCE: 053466/0289 ; CURRENT FILING DATE: 2000-09-29 ; PRIOR APPLICATION NUMBER: US/09/647, 468 ; PRIORITY FILING DATE: 1999-04-02 ; PRIOR APPLICATION NUMBER: JP 10-91850 ; PRIORITY FILING DATE: 1998-04-03 ; NUMBER OF SEQ ID NOS: 183 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 139 ; LENGTH: 118 ; TYPE: PRT ; ORGANISM: Mus sp. ; FEATURE: ; OTHER INFORMATION: Amino acid sequence of H chain v region of anti-TF ; OTHER INFORMATION: mouse monoclonal antibody ATR-2 ; US-09-647-468-139
2	560..5	86.5	118 4	US-09-647-468-140	Sequence 140, APP	Query Match Best Local Similarity 86.5%; Score 560.5; DB 4; length 118; Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;
3	560..5	86.5	137 4	US-09-647-468-153	Sequence 153, APP	QY 1 EIQLOQSGPVELVKPGASVKVSKASGVFTNPNMWWKQSHGSKLSLEWIGYIDPYGDPGY 60 Db 1 BIQLOQSGPVELVKPGASVKVSKASGVFTNPNMWWKQSHGSKLSLEWIGYIDPYGDTY 60
4	560..5	86.5	137 4	US-09-647-468-154	Sequence 154, APP	
5	529..5	81.7	116 2	US-09-647-468-155	Sequence 155, APP	
6	512..5	79.1	118 4	US-09-647-468-144	Sequence 144, APP	
7	512..5	79.1	137 4	US-09-647-468-158	Sequence 158, APP	
8	509..5	78.6	135 1	US-09-647-468-159	Sequence 159, APP	
9	509..5	78.6	135 2	US-09-647-468-159	Sequence 159, APP	
10	503..5	77.7	116 2	US-09-672-345C-105	Sequence 105, APP	
11	503..5	77.7	116 3	US-09-214-095D-90	Sequence 90, APP	
12	503..5	77.7	118 4	US-09-647-468-143	Sequence 143, APP	
13	503..5	77.7	137 4	US-09-647-468-157	Sequence 157, APP	
14	498..5	76.9	116 1	US-09-672-345C-14	Sequence 14, APP	
15	498..5	76.9	116 3	US-09-214-095D-14	Sequence 14, APP	
16	495..5	76.5	116 2	US-09-672-345C-106	Sequence 106, APP	
17	494..5	76.3	137 2	US-09-438-562-3	Sequence 3, APP	
18	494..5	76.3	137 2	US-09-483-528B-93	Sequence 3, APP	
19	494..5	76.3	137 2	US-09-483-528B-93	Sequence 93, APP	
20	494..5	76.3	139 2	US-09-438-562-1	RESULT 2 US-09-647-468-140 ; Sequence 140, Application US/09647468 ; Patent No. 6677436 ; GENERAL INFORMATION: ; APPLICANT: SATO, KOH ; ATTORNEY: ADACHI, HIDEKI ; APPLICANT: YABUTA, NAOHIRO ; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND	
21	494..5	76.3	139 2	US-09-438-528B-91	Sequence 1, APP	
22	494..5	76.3	139 2	US-09-438-528B-91	Sequence 91, APP	
23	492	75.9	117 2	US-09-814-806-4	Sequence 4, APP	
24	492	75.9	117 4	US-09-293-854-4	Sequence 4, APP	
25	490..5	75.7	116 1	US-09-634-278-56	Sequence 56, APP	
26	490..5	75.7	116 1	US-09-777-28-56	Sequence 56, APP	
27	490..5	75.7	116 1	US-09-474-040-56	Sequence 56, APP	

TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY

FILE REFERENCE: 053466/0289

CURRENT APPLICATION NUMBER: US/09/647,468

CURRENT FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: PCT/JP99/01768

PRIOR FILING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 183

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 140

LENGTH: 118

TYPE: PRT

ORGANISM: Mus sp.

FEATURE:

OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF

US-09-647-468-140

Query Match

86.5%; Score 560.5; DB 4; Length 118;

Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY

1 EIQLOQSGPPELVKPGASVYKVSCKASGYAFTINMYWKGSHGKSLWIGTYDPYGDPCY 60

Db

1 EIQLOQSGPPELVKPGASVYKVSCKASGYAFTINMYWKGSHGKSLWIGTYDPYGDPCY 60

QY

61 SQKFKGKATLTVDKSSSTAFMHLNSLSDSAVYCARGE-GYIYDYGQGTITVSS 119

Db

61 SQKFKGKATLTVDKSSSTAFMHLNSLSDSAVYCARGE-GYIYDYGQGTITVSS 118

RESULT 3

US-09-647-468-153

; Sequence 153; Application US/09647468

; Patent No. 6677436

; GENERAL INFORMATION:

; APPLICANT: SATO, KOH

; APPLICANT: ADACHI, HIROKI

; APPLICANT: YABUTA, NAOHIRO

; APPLICANT: SATO, KOH

; APPLICANT: ADACHI, HIROKI

; APPLICANT: YABUTA, NAOHIRO

; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND

; FILE REFERENCE: 053466/0289

; CURRENT APPLICATION NUMBER: US/09/647,468

; PRIOR APPLICATION NUMBER: PCT/JP99/01768

; PRIOR FILING DATE: 1998-04-02

; PRIOR APPLICATION NUMBER: JP 10-91850

; NUMBER OF SEQ ID NOS: 183

; SOFTWARE: PatentIn Ver. 2.1

; LENGTH: 137

; TYPE: PRT

; ORGANISM: Mus sp.

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Amino acid

; US-09-647-468-154

Query Match

86.5%; Score 560.5; DB 4; Length 137;

Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY

1 EIQLOQSGPPELVKPGASVYKVSCKASGYAFTINMYWKGSHGKSLWIGTYDPYGDPCY 60

Db

20 EIQLOQSGPPELVKPGASVYKVSCKASGYAFTINMYWKGSHGKSLWIGTYDPYGDPCY 60

QY

61 SQKFKGKATLTVDKSSSTAFMHLNSLSDSAVYCARGE-GYIYDYGQGTITVSS 119

Db

80 SQKFKGKATLTVDKSSSTAFMHLNSLSDSAVYCARGE-GYIYDYGQGTITVSS 137

RESULT 4

US-09-647-468-154

; Sequence 154; Application US/09647468

; Patent No. 6677436

; GENERAL INFORMATION:

; APPLICANT: SATO, KOH

; APPLICANT: ADACHI, HIROKI

; APPLICANT: YABUTA, NAOHIRO

; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND

; FILE REFERENCE: 053466/0289

; CURRENT APPLICATION NUMBER: US/09/647,468

; PRIOR APPLICATION NUMBER: PCT/JP99/01768

; PRIOR FILING DATE: 1998-04-02

; PRIOR APPLICATION NUMBER: JP 10-91850

; NUMBER OF SEQ ID NOS: 183

; SOFTWARE: PatentIn Ver. 2.1

; LENGTH: 137

; TYPE: PRT

; ORGANISM: Mus sp.

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Amino acid

; US-09-647-468-153

Query Match

86.5%; Score 560.5; DB 4; Length 137;

Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY

1 EIQLOQSGPPELVKPGASVYKVSCKASGYAFTINMYWKGSHGKSLWIGTYDPYGDPCY 60

Db

20 EIQLOQSGPPELVKPGASVYKVSCKASGYAFTINMYWKGSHGKSLWIGTYDPYGDPCY 60

QY

61 SQKFKGKATLTVDKSSSTAFMHLNSLSDSAVYCARGE-GYIYDYGQGTITVSS 119

Db

80 SQKFKGKATLTVDKSSSTAFMHLNSLSDSAVYCARGE-GYIYDYGQGTITVSS 137

RESULT 5

US-08-273-146-55

; Sequence 55; Application US/08273146

; Patent No. 5055855

; GENERAL INFORMATION:

; APPLICANT: Smith, Rodger

; APPLICANT: McCafferty, John

; APPLICANT: Chiswell, David

; APPLICANT: Darst, Michael J.

; APPLICANT: Fitzgerald, Kevin

; APPLICANT: Kenten, John H.

; APPLICANT: Martin, Mark T.

; APPLICANT: Titmuss, Richard C.

; APPLICANT: Williams, Richard O.

; TITLE OF INVENTION: The Isolation and Production of

; NUMBER OF SEQUENCES: 71

; CORRESPONDENCE ADDRESS:

; ADDRESS: IGEN, Inc.

; STREET: 1530 East Jefferson St.

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20852

COMPUTER READABLE FORM:

COMPUTER TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/273, 146

FILING DATE: 14-JUL-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ryan, John W.

REGISTRATION NUMBER: 33,771

REFERENCE/DOCKET NUMBER: 09000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-230-0158

TELEFAX: 301-984-8000

INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: protein

US-08-273-146-55

Query Match 81.7%; Score 529.5; DB 2; Length 116;
Best Local Similarity 85.7%; Pred. No. 1e-43; Matches 102; Conservative 6; Mismatches 8; Indels 3; Gaps 2;

Oy 1 BIQLOQSGPVLVKPGASVSKCASKGAYAFTNNYMWKOSHGSLEWIGYIDPYGCGY 60

Db 1 QVQLOQSGPVLVKPGASVSKCASKGAYAFTNNYMWKOSHGSLEWIGYIDPYGCGY 60

Oy 61 SOKFKGKATLTVDKSSSTAMHNLSTSSESAVYCARRGNNPYFDYQMGQTITVSS 119

Db 61 NOKFKGKATLTVDKSSSTAMHNLSTSSESAVYCAR--GQNP-RPAFWNGQTITVSS 116

RESULT 6 US-09-647-468-144

; Sequence 144, Application US/09647468

; Patent No. 667736

; GENERAL INFORMATION:

; APPLICANT: SATO, KOH

; ATTORNEY: ADACHI, HIDEKI

; APPLICANT: YABUTA, NAOHIRO

; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND

; TITLE OF INVENTION: PROCESS OR PRODUCTION OF THE HUMANIZED ANTIBODY

; FILE REFERENCE: 05346/0289

; CURRENT APPLICATION NUMBER: US/09/647,468

; CURRENT FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: PCT/JP99/01768

; PRIOR FILING DATE: 1999-04-02

; PRIOR APPLICATION NUMBER: JP 10-91850

; PRIOR FILING DATE: 1998-04-03

; NUMBER OF SEQ ID NOS: 183

; SEQ ID NO: 144

; SOFTWARE: PatentIn Ver. 2.1

; LENGTH: 118

; TYPE: PRT

; ORGANISM: Mus sp.

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

; TITLE OF INVENTION: Sequence coding for H chain V region of ant-TF

; OTHER INFORMATION: mouse monoclonal antibody ATR-8

; OTHER INFORMATION: mouse monoclonal antibody ATR-8

; SEQ ID NO: 158

; LENGTH: 137

; TYPE: PRT

; ORGANISM: Mus sp.

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

; TITLE OF INVENTION: Sequence coding for H chain V region of ant-TF

; OTHER INFORMATION: mouse monoclonal antibody ATR-8

; SEQ ID NO: 158

; LENGTH: 137

; TYPE: PRT

; ORGANISM: Mus sp.

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

; TITLE OF INVENTION: Sequence coding for H chain V region of ant-TF

; OTHER INFORMATION: mouse monoclonal antibody ATR-8

Query Match 79.1%; Score 512.5; DB 4; Length 137;
Best Local Similarity 81.3%; Pred. No. 5.3e-42; Matches 98; Conservative 10; Mismatches 9; Indels 3; Gaps 2;

Oy 1 BIQLOQSGPVLVKPGASVSKCASKGAYAFTNNYMWKOSHGSLEWIGYIDPYGCGY 60

Db 20 DIQLOQSGPVLVKPGASVSKCASKGYSFTDYNIFWKOSHGSLEWIGYIDPYGCGY 79

Oy 61 SOKFKGKATLTVDKSSSTAMHNLSTSSESAVYCARRGNNPYFDYQMGQTITVSS 119

Db 80 NOKFKGKATLTVDKSSSTAMHNLSTSSESAVYCAR--GQNP-RPAFWNGQTITVSS 137

RESULT 8 US-08-137-117D-27

; Sequence 27, Application US/08137117D

; Patent No. 5795065

; GENERAL INFORMATION:

; APPLICANT: TSUCHIYA, Masayuki

; APPLICANT: SATO, Koh

; APPLICANT: BENDIG, Mary

; APPLICANT: JONES, Steven

; APPLICANT: SALDANA, Jose

; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR

; NUMBER OF SEQUENCES: 158

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/137,117D

; FILING DATE: 20-DEC-1993

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/JP92/00544

; FILING DATE: 24-APR-1992

RESULT 7

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476

FILING DATE: 25-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.

REFERENCE/DOCKET NUMBER: 25-258

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 135 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-137-117D-27

Query Match 78.6%; Score 509.5; DB 1; Length 135;
Best Local Similarity 80.7%; Pred. No. 1e-41; Mismatches 96; Conservative 11; Indels 3; Gaps 1;

Matches 96; Conservatve 11; Mismatches 9; Indels 3; Gaps 1;

Qy 1 EIQLOQSGPELUKPGASVVKSCASGVAFTINNMVWVKOSHGSLEWIGYIDPYGDGY 60
Db 20 EIQLOQSGPELUKPGASVVKSCASGVAFTINNMVWVKOSHGSLEWIGYIDPYGDGY 79Qy 61 SOKFKGKATLTDKSSTAYMHLNSTSDEAVYCARGRNFYPYFDWKGQGRTLVSS 119
Db 80 NOKFKGKATLTDKSSTAYMHLNSTSDEAVYCARGRNFYPYFDWKGQGRTLVSA 135

RESULT 9

US-08-436-717-27

Sequence 27, Application US/08436717

Patent No. 5817790

GENERAL INFORMATION:

APPLICANT: ISUCHIYA, Masayuki

APPLICANT: SATO, Koh

APPLICANT: BENDIG, Mary

APPLICANT: JONES, Steven

APPLICANT: SALANDRA, Joe

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,717

FILING DATE: 24-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28-678

REFERENCE/DOCKET NUMBER: 0575/51400

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400

TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-672-345C-105

Query Match 78.6%; Score 509.5; DB 2; Length 135;
Best Local Similarity 80.7%; Pred. No. 1e-41; Mismatches 96; Conservative 11; Indels 3; Gaps 1;

Matches 96; Conservatve 11; Mismatches 9; Indels 3; Gaps 1;

Qy 1 EIQLOQSGPELUKPGASVVKSCASGVAFTINNMVWVKOSHGSLEWIGYIDPYGDGY 60
Db 20 EIQLOQSGPELUKPGASVVKSCASGVAFTINNMVWVKOSHGSLEWIGYIDPYGDGY 79Qy 61 SOKFKGKATLTDKSSTAYMHLNSTSDEAVYCARGRNFYPYFDWKGQGRTLVSS 119
Db 80 NOKFKGKATLTDKSSTAYMHLNSTSDEAVYCARGRNFYPYFDWKGQGRTLVSA 135

RESULT 10

US-08-672-345C-105

Sequence 105, Application US/08672345C

Patent No. 5948658

GENERAL INFORMATION:

APPLICANT: Landry Donald, W.

TITLE OF INVENTION: ANTI-COCAINA CATALYTIC ANTIBODY

NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:

ADRESSEE: Cooper and Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C

FILING DATE: 24-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28-678

REFERENCE/DOCKET NUMBER: 0575/51400

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400

TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-672-345C-105

Query Match 77.7%; Score 503.5; DB 2; Length 116;
Best Local Similarity 79.8%; Pred. No. 3.2e-41;

RESULT 11
US-09-214-095D-90
; Sequence 90, Application US/09214095D
; Patent No. 6280387
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAIN CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 90
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Murine
; US-09-214-095D-90

Query Match 77.7%: Score 503.5; DB 3; Length 116;
Best local similarity 79.8%; Pred. No. 3.2e-41; Mismatches 95; Conservative 11; Indels 3; Gaps 1;
Matches 10;

Qy 1 BIOLQSGSPRELVKPGASVKSCKASGKAYFTNNYMWKOSHGSLEWIGYIDPYGDPGY 60
Db 1 EHLQSGSPRELVKPGASVKSCKASGKAYFTNNYMWKOSHGSLEWIGYIDPHNGIFY 60

Qy 61 SQPKKGATLVDKSSSTAYMHNLNSLTSEDSAVYCARGRNFPYFDYWGQTTLVSS 119
Db 61 NOKFKGRATLVDKSSSTAYMHNLNSLTSEDSAVYCAR--GFYDDCYWGQTLTVSA 116

RESULT 12
US-09-647-468-143
; Sequence 143, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647-468-143
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 157
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for H chain V region of anti-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-7
; OTHER INFORMATION: sequence coding for H chain V region of anti-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-7

Query Match 77.7%: Score 503.5; DB 4; Length 137;
Best Local Similarity 80.0%; Pred. No. 3.9e-41; Mismatches 96; Conservative 11; Indels 3; Gaps 1;
Matches 10;

Qy 1 BIOLQSGSPRELVKPGASVKSCKASGKAYFTNNYMWKOSHGSLEWIGYIDPYGDPGY 60
Db 20 DILQSGSPRELVKPGASVKSCKASGKAYFTNNYMWKOSHGSLEWIGYIDPYGSGFY 79

Qy 61 SQPKKGATLVDKSSSTAYMHNLNSLTSEDSAVYCARGRNFPYFDYWGQTTLVSS 119
Db 80 NOKFKGRATLVDKSSSTAYMHNLNSLTSEDSAVYCAR--GFYDDCYWGQTLTVSA 117

RESULT 13
US-09-647-468-157
; Sequence 157, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647-468-157
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 157
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for H chain V region of anti-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-7

Query Match 77.7%: Score 503.5; DB 4; Length 137;
Best Local Similarity 80.0%; Pred. No. 3.9e-41; Mismatches 96; Conservative 11; Indels 3; Gaps 2;
Matches 10;

Qy 1 BIOLQSGSPRELVKPGASVKSCKASGKAYFTNNYMWKOSHGSLEWIGYIDPYGDPGY 60
Db 20 DILQSGSPRELVKPGASVKSCKASGKAYFTNNYMWKOSHGSLEWIGYIDPYGSGFY 79

Qy 61 SQPKKGATLVDKSSSTAYMHNLNSLTSEDSAVYCARGRNFPYFDYWGQTTLVSS 119
Db 80 NOKFKGRATLVDKSSSTAYMHNLNSLTSEDSAVYCAR--GFYDDCYWGQTLTVSA 117

RESULT 14
US-08-672-345C-14
; Sequence 14, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAIN CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:

Query Match 77.7%: Score 503.5; DB 4; length 118;
Best Local Similarity 80.0%; Pred. No. 3.2e-41;
Matches 96; Conservative 11; Mismatches 10; Indels 3; Gaps 2;

APPLICATION NUMBER: US/08/672,345C
 FILING DATE: 24-JUN-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REFERENCE/DOCKET NUMBER: 0575/51400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-672-345C-14

RESULT 15

Query Match 76.9%; Score 498.5; DB 2; Length 116;
 Best Local Similarity 79.7%; Pred. No. 9.6e-41;
 Matches 94; Conservative 10; Mismatches 11; Indels 3; Gaps 1;

Qy 1 EIQLOQSGPPELUVKPGASVKSCKASGIAFPNNWVKQSHGKSLIEWIGYIDPSNGGIFY 60
 Db 1 DVQLOQSGPPELUVKPGASVKSCKASGIAFPNNWVKQSHGKSLIEWIGYIDPSNGGIFY 60

Qy 61 SOKFKGKALTVDKSSTAVWHNLSITSEDSAVVYCARRNFPYFDWYQGQTILTVS 118
 Db 61 NQKFKGKALTVDKSNTAFLHNSLTSBESAVVYCARGGGL--FAWQGQTILTVS 115

US-09-214-095D-14

; Sequence 14, Application US/09214095D
 ; Patent No. 6280987
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald
 ; TITLE OF INVENTION: ANTI-COCAIN CATALYTIC ANTIBODY
 ; FILE REFERENCE: 51400-A-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/214,095D
 ; CURRENT FILING DATE: 1999-07-19
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 14
 ; LENGTH: 116
 ; TYPE: PRT
 ; ORGANISM: Murinae gen. sp.
 ; US-09-214-095D-14

Query Match 76.9%; Score 498.5; DB 3; Length 115;
 Best Local Similarity 79.7%; Pred. No. 9.6e-41;
 Matches 94; Conservative 10; Mismatches 11; Indels 3; Gaps 1;

Qy 1 EIQLOQSGPPELUVKPGASVKSCKASGIAFPNNWVKQSHGKSLIEWIGYIDPSNGGIFY 60
 Db 1 DVQLOQSGPPELUVKPGASVKSCKASGIAFPNNWVKQSHGKSLIEWIGYIDPSNGGIFY 60

Qy 61 SOKFKGKALTVDKSSTAVWHNLSITSEDSAVVYCARRNFPYFDWYQGQTILTVS 118
 Db 61 NQKFKGKALTVDKSNTAFLHNSLTSBESAVVYCARGGGL--FAWQGQTILTVS 115

Search completed: December 29, 2004, 18:08:58
 Job time : 22.5354 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 29, 2004, 17:47:08 ; Search time 20.5354 seconds
(without alignments)
384.304 Million cell updates/sec

Title: US-10-774-076-12
Perfect score: 642
Sequence: 1. EVQLVQSGAVKKPGASVKT.....GNFPYFYDYGQSTLTVTWS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 Seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AAI:
1: /cgnd_6/ptodata/1/iaa/5A_COMB.pep:**
2: /cgnd_6/ptodata/1/iaa/5B_COMB.pep:**
3: /cgnd_5/ptodata/1/iaa/6A_COMB.pep:**
4: /cgnd_6/ptodata/1/iaa/6B_COMB.pep:**
5: /cgnd_6/ptodata/1/iaa/PCTUS_COMB.pep:**
6: /cgnd_5/ptodata/1/iaa/backfiles1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	497.5	77.5	135	1	US-08-137-117D-102		Sequence 102, App
2	497.5	77.5	135	2	US-08-137-117D-102		Sequence 102, App
3	496.5	77.3	116	2	US-08-137-117D-102		Sequence 41, App
4	496.5	77.3	116	5	PCT-US95-01219-41		Sequence 41, App
5	491.5	76.6	135	1	US-08-137-117D-100		Sequence 100, App
6	491.5	76.6	135	2	US-08-137-117D-100		Sequence 57, App
7	488.5	76.1	116	1	US-08-137-278-57		Sequence 57, App
8	488.5	76.1	116	1	US-08-137-634-278-73		Sequence 57, App
9	488.5	76.1	116	1	US-08-137-728-57		Sequence 57, App
10	488.5	76.1	116	1	US-08-137-728-73		Sequence 57, App
11	488.5	76.1	116	1	US-08-137-728-73		Sequence 57, App
12	488.5	76.1	116	1	US-08-137-728-73		Sequence 57, App
13	488.5	76.1	116	1	US-08-137-728-73		Sequence 57, App
14	488.5	76.1	116	1	US-08-137-728-73		Sequence 57, App
15	488.5	76.1	116	3	US-08-137-728-73		Sequence 57, App
16	488.5	76.1	116	3	US-08-137-728-73		Sequence 57, App
17	483.5	75.3	115	1	US-08-137-728-55		Sequence 55, App
18	483.5	75.3	116	1	US-08-137-728-55		Sequence 55, App
19	483.5	75.3	116	1	US-08-137-728-55		Sequence 55, App
20	483.5	75.3	115	1	US-08-137-728-55		Sequence 55, App
21	483.5	75.3	116	1	US-08-137-728-55		Sequence 55, App
22	483.5	75.3	116	1	US-08-137-728-55		Sequence 55, App
23	483.5	75.3	115	1	US-08-137-728-55		Sequence 55, App
24	483.5	75.3	116	1	US-08-137-728-55		Sequence 55, App
25	483.5	75.3	116	2	US-08-137-728-55		Sequence 55, App
26	483.5	75.3	116	2	US-08-137-728-55		Sequence 55, App
27	483.5	75.3	116	2	US-08-137-728-55		Sequence 55, App

ALIGNMENTS

RESULT 1
US-08-137-117D-102
; Sequence 102, Application US/08137117D
; Patent No. 575965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENIGI, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 102:
; LENGTH: 135 amino acids
; TYPE: amino acid

Query Match ; TOPLOGY: linear
 US-08-137-117D-102 ; MOLECULE TYPE: protein

Query Match ; Best Local Similarity 77.5%; Score 497.5; DB 2; Length 135;
 Best Local Similarity 79.0%; Pred. No. 2.1e-40; DB 1; Length 135;
 Matches 94; Conservative 11; Mismatches 11; Indels 3; Gaps 1;

QY 1 EVOLVOSGAEVKPGASVKISCKVSYAFTNMWVRQPGKLEWIGIDPYGDPGY 60
 Db 20 QVOLVOSGAEVKPGASVKISCKVSYAFTNMWVRQPGKLEWIGIDPYGDPGY 60
 QY 61 SOKFKKATLTVDKSTTAYMELSSRLSEDATTAVYCARGNRNPFYFYDFWQGQLVTSS 119
 Db 80 NOKFKKVTMVTDTSTNTAYMELSSRLSEDATTAVYCARGNRNPFYFYDFWQGQLVTSS 135

RESULT 2
 US-08-436-717-102
 ; Sequence 102, Application US/08436717
 ; Patent No. 5817790
 ; GENERAL INFORMATION:
 ; APPLICANT: TSUCHIYA, Masayuki
 ; APPLICANT: SATO, Koh
 ; APPLICANT: BENDIG, Mary
 ; APPLICANT: JONES, Steven
 ; APPLICANT: SALDANHA, Jose
 ; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
 ; NUMBER OF SEQUENCES: 158
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/436,717
 ; FILING DATE: CLASSIFICATION: 536
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/137,117
 ; FILING DATE: 220-DEC-1993
 ; APPLICATION NUMBER: -WO RCT/JP92/00544
 ; FILING DATE: 24-APR-1992
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 4-32084
 ; FILING DATE: 19-FEB-1992
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 3-95476
 ; FILING DATE: 25-APR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WEGNER, Harold C.
 ; REGISTRATION NUMBER: 25,258
 ; INFORMATION FOR SEQ ID NO: 102:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 116 amino acids
 ; STRANDBENDNESS: single
 ; TOPOLOGY: linear
 ; REGISTRATION NUMBER: 25,258
 ; REFERENCE DOCKET NUMBER: 53466/126/AAOK
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEX: 904135
 ; INFORMATION FOR SEQ ID NO: 102:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 135 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

RESULT 3
 US-08-561-521-41
 ; Sequence 41, Application US/08561521
 ; Patent No. 5840299
 ; GENERAL INFORMATION:
 ; APPLICANT: Bendig, Mary M.
 ; APPLICANT: Sieger, Olivier J.
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Jones, S. Tarran
 ; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: One Market Plaza, Stewart Tower, Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/561,521
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/186,269A
 ; FILING DATE: 25-JAN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William L.
 ; REGISTRATION NUMBER: 30,223
 ; REGISTRATION NUMBER: 15270-14
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-543-8600
 ; TELEX: 415-543-503
 ; INFORMATION FOR SEQ ID NO: 41:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 116 amino acids
 ; STRANDBENDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

RESULT 4
 US-08-561-521-41
 ; Query Match
 ; Best Local Similarity 77.3%; Score 496.5; DB 2; Length 116;
 ; Matches 93; Conservative 12; Mismatches 11; Indels 3; Gaps 1;

QY 1 EVOLVOSGAEVKPGASVKISCKVSYAFTNMWVRQPGKLEWIGIDPYGDPGY 60
 Db 1 QVOLVOSGAEVKPGASVKISCKVSYAFTNMWVRQPGKLEWIGIDPYGDPGY 60
 QY 61 SOKFKKATLTVDKSTTAYMELSSRLSEDATTAVYCARGNRNPFYFYDFWQGQLVTSS 119
 Db 61 SOKFKKVTMVTDTSTNTAYMELSSRLSEDATTAVYCARGNRNPFYFYDFWQGQLVTSS 135

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,717

FILING DATE: 24-APR-1992

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476

FILING DATE: 25-APR-1991

ATTORNEY / AGENT INFORMATION:

NAME: WEGNER, Harold C.

REGISTRATION NUMBER: 25, 258

REFERENCE/DOCKET NUMBER: 53,466/126/AOK

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5399

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: peptide

US-08-436-717-100

Query Match 76.6%; Score 491.5; DB 2; Length 135;

Best Local Similarity 77.3%; Pred. No. 8.1e-40; Matches 92; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

Qy 1 EVOLVOSGAEVTKPGASVKISKVSGYAFINNMWVROAAGPKGLEMWGIVPPYCPGY 60

Db 20 QVOLVOSGAEVTKPGASVKISKVSGYAFINNMWVROAAGPKGLEMWGIVPPYCPGY 60

Qy 61 SQKFKGKATITVDKSTSTAYMEELSLRSIDTAVYCARGRNFYYFDWQGQTLTVSS 119

Db 80 NQKFKGKVMTVDISTNTAYMEELSLRSIDTACYCARGRGN--RFAYWQGTNLTVSS 135

RESULT 7
US-07-634-278-57

Sequence 57, Application US/07634278

Patent No. 5530101

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLFI, Nicholas F.

APPLICANT: COELINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 11823-002600
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2422
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLogy: linear
MOLECULE TYPE: peptide

US-07-634-278-57

Query Match 76.1%; Score 488.5; DB 1; Length 116;

Best Local Similarity 79.0%; Pred. No. 1.3e-39; Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

Qy 1 EVOLVOSGAEVTKPGASVKISKVSGYAFINNMWVROAAGPKGLEMWGIVPPYCPGY 60

Db 1 QVOLVOSGAEVTKPGSSVKISKVSGYFTDYNHMWVROAAGPKGLEMWGIVPPYCPGY 60

Qy 61 SQKFKGKATITVDKSTSTAYMEELSLRSIDTAVYCARGRNFYYFDWQGQTLTVSS 119

Db 61 NQKFKGKVMTVDISTNTAYMEELSLRSIDTACYCARGRNFYYFDWQGQTLTVSS 116

RESULT 8
US-07-634-278-73

Sequence 73, Application US/07634278

Patent No. 5530101

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLFI, Nicholas F.

APPLICANT: COELINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278

FILING DATE: 19-DEC-1990

CLASSIFICATION: 424
PRIOR APPLICATION DATA:

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 STRANDBEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-477-728-73

Query Match 76.1%; Score 488.5; DB 1; Length 116;
 Best Local Similarity 79.0%; Pred. No. 1.3e-39;
 Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

Qy 1 EVOLVOSCAEVKKPGASVKISKVSKVSGYAFPTNMYWVQRQPKGLEWIGYIDPYGPGY 60
 Db 1 QVOLVOSCAEVKKPGSSVKISKVSKVSGYAFPTNMYWVQRQPKGLEWIGYIDPYGPGY 60

Qy 61 SQKPKGKATLTDKSSTAYMELSSRSEDTAVYVCCRARRNFPPYFDYMQGQTLYTVSS 119
 Db 61 NOKPKSQTATADESTNTAYMELSSRSEDTAVYVCCRARRNFPPYFDYMQGQTLYTVSS 116

RESULT 11
 US-08-474-040-57
 Sequence 57, Application US/08474040
 Patent No. 5693761
 GENERAL INFORMATION:
 APPLICANT: QUEEN, Cary L.
 APPLICANT: CO, Man Sung
 APPLICANT: SCHNEIDER, William P.
 APPLICANT: LANDOLFI, Nicholas F.
 APPLICANT: COBLINGH, Kathleen L.
 APPLICANT: SELICK, Harold E.
 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474, 040
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/634, 278
 FILING DATE: 19-DEC-1990
 APPLICATION NUMBER: -US 07/590, 274
 FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310, 252
 FILING DATE: 13-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290, 975
 FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:
 NAME: SMITH, William M
 REGISTRATION NUMBER: 30-223
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 STRANDBEDNESS: Single

Query Match 76.1%; Score 488.5; DB 1; Length 116;
 Best Local Similarity 79.0%; Pred. No. 1.3e-39;
 Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

Qy 1 EVOLVOSCAEVKKPGASVKISKVSKVSGYAFPTNMYWVQRQPKGLEWIGYIDPYGPGY 60
 Db 1 QVOLVOSCAEVKKPGSSVKISKVSKVSGYAFPTNMYWVQRQPKGLEWIGYIDPYGPGY 60

Qy 61 SQKPKGKATLTDKSSTAYMELSSRSEDTAVYVCCRARRNFPPYFDYMQGQTLYTVSS 119
 Db 61 NOKPKSQTATADESTNTAYMELSSRSEDTAVYVCCRARRNFPPYFDYMQGQTLYTVSS 116

RESULT 12
 US-08-474-040-73
 Sequence 73, Application US/08474040
 Patent No. 5693761
 GENERAL INFORMATION:
 APPLICANT: QUEEN, Cary L.
 APPLICANT: CO, Man Sung
 APPLICANT: SCHNEIDER, William P.
 APPLICANT: LANDOLFI, Nicholas F.
 APPLICANT: COBLINGH, Kathleen L.
 APPLICANT: SELICK, Harold E.
 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474, 040
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/634, 278
 FILING DATE: 19-DEC-1990
 APPLICATION NUMBER: -US 07/590, 274
 FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310, 252
 FILING DATE: 13-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: -US 07/290, 975
 FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:
 NAME: SMITH, William M
 REGISTRATION NUMBER: 30-223
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 STRANDBEDNESS: Single

; MOLECULE TYPE: peptide
; US-08-474-040-73

TOPOLOGY: linear

Query Match 76.1%; Score 488.5; DB 1; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

GENERAL INFORMATION:
Patent No. 5693762
Applicant: QUEEN, Cary L.
Applicant: CO, Man Sung
Applicant: SCHNEIDER, William P.
Applicant: LANDOLFI, Nicholas F.
Applicant: COBLING, Kathleen L.
Applicant: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
ADDRESSEES: Townsend and Townsend and Crew
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-57

RESULT 13
US-08-487-200-57

Sequence 57, Application US/08487200
; Sequence 73, Application US/08487200
; Patent No. 5693762

GENERAL INFORMATION:
Applicant: QUEEN, Cary L.
Applicant: CO, Man Sung
Applicant: SCHNEIDER, William P.
Applicant: LANDOLFI, Nicholas F.
Applicant: COBLING, Kathleen L.
Applicant: SELICK, Harold E.

Title of Invention: IMPROVED HUMANIZED IMMUNOGLOBLINS
Number of Sequences: 113

Correspondence Address:
Addressee: Townsend and Townsend and Crew
Street: 379 Lytton Avenue
City: Palo Alto
State: California
Country: US
Zip: 94301

Computer Readable Form:
Medium Type: Floppy disk
Computer: IBM PC compatible
Operating System: PC-DOS/MS-DOS
Software: Patent In Release #1.0, Version #1.25

Current Application Data:
Application Number: US/08/487,200
Filing Date: 7-JUN-1995
Classification: 424

Prior Application Data:
Application Number: US 07/634,278
Filing Date: 19-DEC-1990

Prior Application Data:
Application Number: US 07/590,274
Filing Date: 28-SEP-1990

Prior Application Data:
Application Number: US 07/310,252
Filing Date: 13-FEB-1989

Prior Application Data:
Application Number: US 07/290,975
Filing Date: 28-DEC-1988

Attorney/Agent Information:
Name: Smith, William M
Registration Number: 30,223
Reference/Docket Number: 11823-002610
Telecommunication Information:
Telephone: (415) 326-2400
Telefax: (415) 326-4422

Information for Seq Id No: 73:
Sequence Characteristics:
Length: 116 amino acids
Type: amino acid
Strandedness: Single
Topology: linear
Molecule Type: peptide
US-08-487-200-73

RESULT 14
US-08-487-200-73

Sequence 73, Application US/08487200
; Sequence 73, Application US/08487200
; Patent No. 5693762

GENERAL INFORMATION:
Applicant: QUEEN, Cary L.
Applicant: CO, Man Sung
Applicant: SCHNEIDER, William P.
Applicant: LANDOLFI, Nicholas F.
Applicant: COBLING, Kathleen L.
Applicant: SELICK, Harold E.

Title of Invention: IMPROVED HUMANIZED IMMUNOGLOBLINS
Number of Sequences: 113

Correspondence Address:
Addressee: Townsend and Townsend and Crew
Street: 379 Lytton Avenue
City: Palo Alto
State: California
Country: US
Zip: 94301

Computer Readable Form:
Medium Type: Floppy disk
Computer: IBM PC compatible
Operating System: PC-DOS/MS-DOS
Software: Patent In Release #1.0, Version #1.25

Current Application Data:
Application Number: US/08/487,200
Filing Date: 7-JUN-1995
Classification: 424

Prior Application Data:
Application Number: US 07/634,278
Filing Date: 19-DEC-1990

Prior Application Data:
Application Number: US 07/590,274
Filing Date: 28-SEP-1990

Prior Application Data:
Application Number: US 07/310,252
Filing Date: 13-FEB-1989

Prior Application Data:
Application Number: US 07/290,975
Filing Date: 28-DEC-1988

Attorney/Agent Information:
Name: Smith, William M
Registration Number: 30,223
Reference/Docket Number: 11823-002610
Telecommunication Information:
Telephone: (415) 326-2400
Telefax: (415) 326-4422

Information for Seq Id No: 73:
Sequence Characteristics:
Length: 116 amino acids
Type: amino acid
Strandedness: Single
Topology: linear
Molecule Type: peptide
US-08-487-200-73

Query Match 76.1%; Score 488.5; DB 1; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

GENERAL INFORMATION:
Patent No. 5693762
Applicant: QUEEN, Cary L.
Applicant: CO, Man Sung
Applicant: SCHNEIDER, William P.
Applicant: LANDOLFI, Nicholas F.
Applicant: COBLING, Kathleen L.
Applicant: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
ADDRESSEES: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-4422

INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-73

RESULT 15
Sequence 57, Application US/08484537-57
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung William P.
APPLICANT: SCHNEIDER, Nicholas P.
APPLICANT: COBLINCH, Kathleen L.
APPLICANT: SHILICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Bayton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: J0.223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPLOGY: linear
MOLECULE TYPE: peptide
US-08-484-537-57

Query Match 76.1%; Score 488.5; DB 3; Length 116;
Best Local Similarity 79.5%; Pred. No. 1.3e-39; Mismatches 10; Indels 3; Gaps 2;
Matches 94; Conservative 10; MisMatches 12; Indels 3; Gaps 2;
1 EVOLVOSGAEVKPGKPGASVTKISKVSGAFTVNMWYMQPKGLEWIGVDPYQDPGY 60

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:47:08 ; Search time 18.4646 Seconds
384.304 Million cell updates/sec

Title: US-10-774-076-3
Perfect score: 563
Sequence: 1. DIKMTSPSSMYASLGERVT.....CLQYDPPFPYTFGGGTIK 107
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : issued_Patents_AA.*

- 1: /cgtr2_6/pctdata/1/1aa/5A-COMB.pep:*
- 2: /cgtr2_6/pctdata/1/1aa/5B-COMB.pep:*
- 3: /cgtr2_6/pctdata/1/1aa/6A-COMB.pep:*
- 4: /cgtr2_6/pctdata/1/1aa/6B-COMB.pep:*
- 5: /cgtr2_6/pctdata/1/1aa/6C-TUS-COMB.pep:*
- 6: /cgtr2_6/pctdata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	551	97.9	355	3 US-08-875-811-41
2	551	97.9	355	3 US-08-875-811-41
3	551	97.9	355	3 US-08-875-811-64
4	551	97.9	358	3 US-08-875-811-45
5	551	97.9	360	3 US-08-875-811-47
6	551	97.9	379	3 US-08-875-811-43
7	546	97.0	127	3 US-08-348-548-4
8	546	97.0	127	5 PCT-US95-15176-4
9	541	96.1	107	1 US-08-107-696D-26
10	541	96.1	107	1 US-08-472-788A-26
11	541	96.1	107	2 US-08-477-531B-26
12	541	96.1	107	2 US-08-082-842A-26
13	541	96.1	107	3 US-09-136-389-123
14	531	94.3	107	1 US-08-425-336-123
15	531	94.3	107	1 US-08-481-113B-123
16	531	94.3	107	1 US-08-477-484B-123
17	531	94.3	107	2 US-08-472-788A-26
18	531	94.3	107	3 US-08-839-765-123
19	531	94.3	107	3 US-09-136-389-123
20	531	94.3	107	3 US-08-610-838-123
21	531	94.3	107	4 US-09-711-485-123
22	527	93.6	107	2 US-08-290-592E-21
23	527	93.6	107	5 PCT-US95-10053-18
24	527	93.6	107	5 PCT-US96-19448-21
25	525	93.3	215	2 US-08-737-129A-8
26	522	92.7	142	2 US-08-979-940-2
27	522	92.7		US-08-838-692-4

ALIGNMENTS

RESULT 1
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 604593
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Luis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Clegg LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOOS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41-739
; REFERENCE/DOCKET NUMBER: 015280-24100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPeLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-41
; Query Match Best Local Similarity 97.9%; Score 551; DB 3; Length 355;

FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Faris, Susan K.
 REGISTRATION NUMBER: 41-739
 REFERENCE/DOCKET NUMBER: 012280-244100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEX/FAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 360 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-875-811-47

Query Match 97.9%; Score 551; DB 3; Length 360;
 Best Local Similarity 97.2%; Pred. No. 8-5e-46;
 Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSSMYSASLGERVITCKASODINSYLSWFOQKGSKPSKPLIYRANRLVGVPS 60
 Db 121 DIKMTQSPSSMYSASLGERVITCKASODINSYLSWFOQKGSKPSKPLIYRANRLVGVPS 180
 Qy 61 RFSGSGSGDYSLTISLEEDMGIVYCYCLODERPYTFGGTKLEIK 107
 Db 181 RFSGSGSGDYSLTISLEEDMGIVYCYCLOQDEFPYTFGGTKLEIK 227
 Db 203 RFSGSGSGDYSLTISLEEDMGIVYCYCLOQDEFPYTFGGTKLEIK 249

RESULT 7

US-08-875-811-43

Sequence 43, Application US/08875811
 Patent No. 6045793
 GENERAL INFORMATION:

APPLICANT: Robak, Susanna M.
 APPLICANT: Newton, Diane L.
 APPLICANT: Bogue, Luis
 APPLICANT: Włodawer, Alexander
 TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0B

CURRENT APPLICATION DATA:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875,811
 FILING DATE: 19-FEB-1998
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/02588
 FILING DATE: 19-FEB-1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/011,800
 FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Faris, Susan K.

REGISTRATION NUMBER: 41-739
 REFERENCE/DOCKET NUMBER: 012280-244100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEX/FAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 379 amino acids
 TYPE: amino acid

MOLECULE TYPE: protein
 US-08-875-811-47

TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-875-811-43

Query Match 97.9%; Score 551; DB 3; Length 379;
 Best Local Similarity 97.2%; Pred. No. 9e-46;
 Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSSMYSASLGERVITCKASODINSYLSWFOQKGSKPSKPLIYRANRLVGVPS 60
 Db 143 DIKMTQSSSMYSASLGERVITCKASODINSYLSWFOQKGSKPSKPLIYRANRLVGVPS 202
 Qy 61 RFSGSGSGDYSLTISLEEDMGIVYCYCLODERPYTFGGTKLEIK 107
 Db 203 RFSGSGSGDYSLTISLEEDMGIVYCYCLOQDEFPYTFGGTKLEIK 249

RESULT 8

US-08-848-548-4

Sequence 4, Application US/08348548
 Patent No. 6259529
 GENERAL INFORMATION:

APPLICANT: Berdoz, Jose
 APPLICANT: Krahenbuhl, Jean Pierre
 TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
 TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
 NUMBER OF SEQUENCES: 108
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street, Suite 3100
 CITY: Boston
 STATE: MA

COUNTRY: USA
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.3.0B
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/348,548

FILING DATE: 01-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REFERENCE NUMBER: 30-162

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEX: 200154

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 127 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-348-548-4

Query Match 97.0%; Score 546; DB 3; Length 127;
 Best Local Similarity 95.3%; Pred. No. 8-2e-46;
 Matches 102; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSSMYSASLGERVITCKASODINSYLSWFOQKGSKPSKPLIYRANRLVGVPS 60
 Db 21 DIKMTQSSSMYSASLGERVITCKASODINSYLSWFOQKGSKPSKPLIYRANRLVGVPS 80
 Qy 61 RFSGSGSGDYSLTISLEEDMGIVYCYCLODERPYTFGGTKLEIK 107
 Db 81 RFSGSGSGDYSLTISLEEDMGIVYCYCLOQDEFPYTFGGTKLEIK 127

RESULT 9

PCT-US95-15716-4
Sequence 4, Application PC/TUS9515716
GENERAL INFORMATION:
APPLICANT: Berdoz, Jose
APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15716
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1993
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbalia
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-107-669D-26
Query Match 97.0%; Score 546; DB 5; Length 127;
Best Local Similarity 95.3%; Pred No. 8.2e-46;
Matches 102; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIKMQTQSPSSMYASIGERVITCKASQDINSYLWFOQKPKGSKPTLIVANRLVDGVPS 60
Db 21 DIKMQTQSPSSMYASIGERVITCKASQDINSYLWFOQKPKGSKPTLIVANRLVDGVPS 60
QY 61 RFSSGGSGQDYSLTISLEYEDMGIVYCLQYDPRPYTGGTKLIK 107
Db 61 RFSSGGSGQDYSLTISLEYEDMGIVYCLQYDPRPYTGGTKLIK 107
RESULT 11
US-08-472-788A-26
Sequence 26, Application US/08472788A
Patent No. 570196
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESS: Stern, Kessler, Goldstein and Fox P. L. L. C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472-788A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464

FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33_851
REFERENCE/DOCKET NUMBER: 0610.1000003
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-788A-26

Query Match ;
Best Local Similarity 96.1%; Score 541; DB 1; Length 107;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIKMTQSPPSSMVASLGERVTICKASODINSVLSWFOQPKGSKSPKTLIYRANLVGVPS 60
Db 1 DIKMTQSPPSSMVASLGERVTICKASODINSVLSWFOQPKGSKSPKTLIYRANLVGVPS 60

Qy 61 RFSGSGSGQDYSLTISLEEDMGIVYCLQDEFPYTFGGTKLIRK 107
Db 61 RFSGSGSGQDYSLTISLEEDMGIVYCLQDEFPYTFGGTKLIRK 107

RESULT 12
US-08-477-531B-26.

Sequence 26 Application US/08477531B
Patent No. 5821123

GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,842A
FILING DATE: 23-JUN-1993
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33_851
REFERENCE/DOCKET NUMBER: 0610.1000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-082-842A-26

Query Match ;
Best Local Similarity 96.1%; Score 541; DB 2; Length 107;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIKMTQSPPSSMVASLGERVTICKASODINSVLSWFOQPKGSKSPKTLIYRANLVGVPS 60
Db 1 DIKMTQSPPSSMVASLGERVTICKASODINSVLSWFOQPKGSKSPKTLIYRANLVGVPS 60

Qy 61 RFSGSGSGQDYSLTISLEEDMGIVYCLQDEFPYTFGGTKLIRK 107

RESULT 13
US-08-082-842A-26
Sequence 26 Application US/08082842A
Patent No. 5839619

GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,842A
FILING DATE: 23-JUN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33_851
REFERENCE/DOCKET NUMBER: 0610.1000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-082-842A-26

Query Match ;
Best Local Similarity 96.1%; Score 541; DB 2; Length 107;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIKMTQSPPSSMVASLGERVTICKASODINSVLSWFOQPKGSKSPKTLIYRANLVGVPS 60
Db 1 DIKMTQSPPSSMVASLGERVTICKASODINSVLSWFOQPKGSKSPKTLIYRANLVGVPS 60

Qy 61 RFSGSGSGQDYSLTISLEEDMGIVYCLQDEFPYTFGGTKLIRK 107

Db 61 RPSGSGSGDYSLTISLVEDMGIVYQCYQYDESPWTFCGGTKLEIK 107

RESULT 14

US-08-425-336-123

; Sequence 123, Application US/08425336

; Patent No. 5621083

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

; NUMBER OF SEQUENCES: 140

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

; STREET: 500 West Madison Street, 34th floor

; CITY: Chicago

; STATE: Illinois

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/425,336

FILING DATE: 18-APR-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/064,691

FILING DATE: 12-MAY-1993

ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: -US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Thomas C.

REGISTRATION NUMBER: P-36,989

REFERENCE/DOCKET NUMBER: 31394

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 123:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: protein

US-08-425-336-123

Query Match 94.3%; Score 531; DB 1; Length 107;

Best Local Similarity 94.4%; Pred. No. 1.9e-44; Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIKMTQSSPSSMYASIGERVTITCKASODINSYLSWFOQKPGKSPKTLYRANRLVDPVS 60

Db 1 DIKMTQSSPSSMYASIGERVTITCKASODINSYLSWFOQKPGKSPKTLYRANRLVDPVS 60

QY 61 RPSGSGSGDYSLTISLVEDMGIVYQCYQYDESPWTFCGGTKLEIK 107

Db 61 RPSGSGSGDYSLTISLVEDMGIVYQCYQYDESPWTFCGGTKLEIK 107

Db 61 RPSGSGSGDYSLTISLVEDMGIVYQCYQYDESPWTFCGGTKLEIK 107

RESULT 15

US-08-488-113B-123

; Sequence 123, Application US/08488113B

; Patent No. 5744580

Search completed: December 29, 2004, 18:08:59

Job time : 19.464 sec

THIS PAGE BLANK (use reverse)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:47:08 ; Search time 20.0177 Seconds

Scoring table: BLOSUM62 384.304 Million cell updates/sec

Title: US-10-774-076-4

Perfect score: 617

Sequence: 1 BVQLQQSAGELVRSAGSVAL.....YGGTTTAYWGGTGLTVUSA 116

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqb, 66318600 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata1/1/aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata1/1/aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata1/1/aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata1/1/aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata1/1/aa/PCRTS_COMB.pep:*
- 6: /cgn2_6/prodata1/1/aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	52.3	84.8	118	3 US-08-767-128-22 Sequence 22, Appl
2	51.6	83.6	535	3 US-08-983-335A-38 Sequence 38, Appl
3	50.8	82.3	124	1 US-08-017-570-6 Sequence 6, Appl
4	50.8	82.3	124	1 US-08-471-026-6 Sequence 6, Appl
5	50.8	82.3	124	1 US-08-470-909-6 Sequence 6, Appl
6	50.7	82.2	136	4 US-09-564-329A-11 Sequence 11, Appl
7	50.7	82.2	136	4 US-09-963-020-11 Sequence 11, Appl
8	50.7	82.2	136	4 US-09-965-032-11 Sequence 11, Appl
9	50.5	81.8	281	3 US-09-423-439-44 Sequence 44, Appl
10	50.5	81.8	642	3 US-09-423-339-26 Sequence 26, Appl
11	50.5	81.8	666	3 US-09-423-339-51 Sequence 51, Appl
12	50.3	81.5	124	1 US-017-570-4 Sequence 4, Appl
13	50.3	81.5	124	1 US-08-471-026-4 Sequence 4, Appl
14	50.3	81.5	124	1 US-09-364-088-11 Sequence 4, Appl
15	50.2	81.4	255	3 PCT-US94-01709-4 Sequence 19, Appl
16	50.2	81.4	270	2 US-08-652-077-2 Sequence 2, Appl
17	50.1	81.2	553	2 US-08-652-052-16 Sequence 16, Appl
18	50.1	81.2	553	3 US-08-188-082-16 Sequence 16, Appl
19	50.1	81.2	553	3 US-09-364-088-16 Sequence 16, Appl
20	50.1	81.2	553	3 US-09-102-161-16 Sequence 16, Appl
21	50.0	81.0	136	3 US-08-348-548-8 Sequence 8, Appl
22	50.0	81.0	136	5 PCT-US95-15716-8 Sequence 8, Appl
23	498.5	80.8	254	2 US-08-792-024-4 Sequence 4, Appl
24	498.5	80.8	254	2 US-08-792-024-7 Sequence 7, Appl
25	498.5	80.8	254	2 US-08-792-024-10 Sequence 10, Appl
26	498.5	80.8	254	2 US-08-792-024-13 Sequence 13, Appl
27	496	80.4	124	3 US-09-672-009-1 Sequence 1, Appl

RESULT 1
US-08-767-128-22
; Sequence 22, Application US/08767128
; Patent No. 611079
; GENERAL INFORMATION:
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Walter & Schmidt
; STREET: 3100 No. 611079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; PRIORITY APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; PRIORITY APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 10-OCT-1995
; PRIORITY APPLICATION DATA:
; PRIORITY APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carrer, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648 49USP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TYPE: amino acid

STRANDBENESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

US-08-767-128-22

Query Match 84.8%; Score 523; DB 3; Length 118;

Best Local Similarity 86.4%; Pred. No. 2.8e-46; Matches 102; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

Qy 1 EVQLQSGAELVRSAGASVLUCLTASGENIKDYYIHWKQRPEGLEWIGCIPDENGY 60

Db 1 EVQLQSGAELVRSAGASVLUCLTASGENIKDYYIHWKQRPEGLEWIGCIPDENGY 60

Qy 3 QVQLQSGAELVRSAGASVLUCLTASGENIKDYYIHWKQRPEGLEWIGCIPDENGY 62

Db 61 APNFOGRAFTADTSNTAYLQLSLSITSEDATAVYCY--YGGTITFAWMQGQTLVSA 116

Qy 63 APKFGKATMTADTSNTAYLQLSLSITSEDATAVYCYCFYGDLD-YWGQQTIVVS 118

Db 63 APKFGKATMTADTSNTAYLQLSLSITSEDATAVYCYCFYGDLD-YWGQQTIVVS 118

RESULT 2

US-08-983-035A-38

Sequence 38, Application US/08983035A

Patent No. 6326464

GENERAL INFORMATION:

APPLICANT: BRACCO, LAURENT

TITLE OF INVENTION: P3 PROTEIN VARIANTS AND THERAPEUTICAL

NUMBER OF SEQUNECES: 59

GENERAL INFORMATION:

CORRESPONDENCE ADDRESS:

ADDRESSEE: FINNEGAN, HENDERSON, FARROW, GARRETT &

STREET: 1300 I Street, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/983, 035A

FILING DATE: 20-Feb-1998

CLASSIFICATION: UNKNOWN>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/01111

FILING DATE: 17-JUL-1996

APPLICATION NUMBER: FR 95/08729

FILING DATE: 19-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Straus, William L.

REGISTRATION NUMBER: 47,114

REFERENCE/DOCKET NUMBER: 03004.0142

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 535 amino acids

TYPE: amino acid

TOPOLGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Query Match 83.6%; Score 516; DB 3; Length 535;

Best Local Similarity 84.7%; Pred. No. 9.1e-45; Matches 100; Conservative 6; Mismatches 8; Indels 4; Gaps 2;

Qy 1 EVQLQSGAELVRSAGASVLUCLTASGENIKDYYIHWKQRPEGLEWIGCIPDENGY 60

Db 1 EVQLQSGAELVRSAGASVLUCLTASGENIKDYYIHWKQRPEGLEWIGCIPDENGY 60

Qy 3 QVQLQSGAELVRSAGASVLUCLTASGENIKDYYIHWKQRPEGLEWIGCIPDENGY 62

Db 61 APNFOGRAFTADTSNTAYLQLSLSITSEDATAVYCY--YGGTITFAWMQGQTLV 116

Qy 63 APKFGKATMTADTSNTAYLQLSLSITSEDATAVYCYCFYGDLD-YWGQQTIVVS 118

Db 63 APKFGKATMTADTSNTAYLQLSLSITSEDATAVYCYCFYGDLD-YWGQQTIVVS 118

RESULT 3

US-08-017-570-6

Sequence 6, Application US/08017570

Patient No. 5477693

GENERAL INFORMATION:

APPLICANT: COURIE, BRIAN B

APPLICANT: RIXON, MARK W

APPLICANT: MEZES, PETER S

APPLICANT: KAPLAN, DONALD A

APPLICANT: SCHLOM, JEFFREY

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

NUMBER OF SEQUNECES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Diane C. Ulmer

STREET: P.O. Box 1967

CITY: Midland

STATE: MI

COUNTRY: US

ZIP: 48641-1967

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/017,570

FILING DATE: 19930216

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: ULMER, DUANE C

REGISTRATION NUMBER: 34,941

REFERENCE/DOCKET NUMBER: C-38, 777

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids

TYPE: AMINO ACID

TOPOLGY: linear

MOLECULE TYPE: protein

APPLICATION NUMBER: FR 95/08729

FILING DATE: 19-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Straus, William L.

REGISTRATION NUMBER: 47,114

REFERENCE/DOCKET NUMBER: 03004.0142

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TOPOLGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-08-983-035A-38

RESULT 4

US-08-471-426-6

; Sequence 6, Application US/08471426

; Patent No. 5508033

; GENERAL INFORMATION:

; APPLICANT: RIXON, MARK W

; APPLICANT: MEZES, PETER S

; APPLICANT: KAPLAN, DONALD A

; APPLICANT: SCHIOM, JEFFREY

; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSE: Duane C. Ulmer

; STREET: P.O. Box 1967

; CITY: Midland

; STATE: MI

; ZIP: 48641-1967

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/01709

; FILING DATE: 06-JUN-1995

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: ULMER, DUANE C

; REGISTRATION NUMBER: 34,941

; REFERENCE/DOCKET NUMBER: 38,777-F

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (517) 636-8104

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 124 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; PCT-US94-01709-6

; QUERY Match 82.3%; Score 508; DB 1; length 124;

; Best Local Similarity 81.5%; Pred. No. 1e-44; Mismatches 11; Indels 8; Gaps 2;

; Matches 101; Conservative 4; MisMatches 11; Del 8; Gap 2;

; Qy 1 EVOLQSGAELVRSAGSVKLSCTASGFNIKYIHWKORPQEGLWIGCIDIPEGDTY 60

; Db 1 EVOLQSGAELVRSAGSVKLSCTASGFNIKYIHWKORPQEGLWIGCIDIPEGDTY 60

; Qy 1 EVOLQSGAELVRSAGSVKLSCTASGFNIKYIHWKORPQEGLWIGCIDIPEGDTY 60

; Db 1 EVOLQSGAELVRSAGSVKLSCTASGFNIKYIHWKORPQEGLWIGCIDIPEGDTY 60

; Qy 61 APNFGQRATMADTSNTAYQLQSLISLTSEPTAVTC---YGGTIT---PAYNGQGTV 112

; Db 61 APKFQGKATMTDIDSSNTAYQLQSLISLTSEPTAVYCNTRGSLSTMTRWFDFWNGAGTV 120

; Qy 113 TVSA 116

; Db 121 TVSS 124

RESULT 6

US-09-564-329A-11

; Sequence 11, Application US/09564329A

; Patent No. 6541212

; GENERAL INFORMATION:

; APPLICANT: Reiter, Robert E.

; APPLICANT: Witte, Owen N.

; APPLICANT: Saffran, Douglas C.

; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

; FILE REFERENCE: 30415.54US14

; CURRENT APPLICATION NUMBER: US/09/564,329A

; CURRENT FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: 09/359,326

; PRIOR FILING DATE: 1999-07-20

; PRIOR APPLICATION NUMBER: 08/814,279

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: 60/071,141

; PRIOR FILING DATE: 1998-01-12

; PRIOR APPLICATION NUMBER: 60/074,675

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: 60/113,230

; PRIOR APPLICATION NUMBER: 60/120,536

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: 60/124,658

; PRIOR FILING DATE: 1999-03-16

; RESULT 5

PCT-US94-01709-6

; Sequence 6, Application PC/TUS9401709

; GENERAL INFORMATION:

; APPLICANT: THE DOW CHEMICAL COMPANY

; APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES

; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTI-CHIMERIC ANTIBODIES

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

PRIOR FILING DATE: 1998-03-10
 PRIOR FILING DATE: 1998-12-02
 PRIOR APPLICATION NUMBER: 09/251,835
 PRIOR FILING DATE: 1999-02-17
 PRIOR APPLICATION NUMBER: 09/308,503
 PRIOR FILING DATE: 1999-05-25
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 11
 LENGTH: 136
 TYPE: PRT
 ORGANISM: SCID Mice
 US-09-564-329A-11

RESULT 7
 Query Match 82.2%; Score 507; DB 4; Length 136;
 Best Local Similarity 84.5%; Pred. No. 1.5e-44; Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
 Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
 Qy 1 EVOLQOSGAEVLVRSGASVAKLSCTAGSFGNPKDYYIHWKQRPGQLEWIGCIPDENGDTY 60
 Db 14 EVOLQOSGAEVLVRSGASVAKLSCTAGSFGNPKDYYIHWKQRPGQLEWIGCIPDENGDTY 73
 Qy 61 APNFGGRATMADTSNTAYLQLSSITSDTAVYCYGGTIPAYNGQTLVUSA 115
 Db 74 VPKFOQKATMADTSNTAYLQLSSITSDTAVYCYKG---GFWGQGTIVUSA 125

RESULT 7
 Sequence 11, Application US/09963620
 Patient No. 6756036
 GENERAL INFORMATION:
 APPLICANT: Reiter, Robert E.
 APPLICANT: Witte, Owen N.
 APPLICANT: Saffran, Douglas C.
 TITLE OF INVENTION: PSCA, PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 FILE REFERENCE: 39435.54US14
 CURRENT APPLICATION NUMBER: US/09/963,620
 CURRENT FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 09/564,329
 PRIOR FILING DATE: 2000-05-03
 PRIOR APPLICATION NUMBER: 09/359,326
 PRIOR FILING DATE: 1999-07-20
 PRIOR APPLICATION NUMBER: 09/814,279
 PRIOR FILING DATE: 1997-03-10
 PRIOR APPLICATION NUMBER: 60/071,141
 PRIOR FILING DATE: 1998-01-12
 PRIOR APPLICATION NUMBER: 60/074,675
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: 60/113,230
 PRIOR FILING DATE: 1998-12-21
 PRIOR APPLICATION NUMBER: 60/120,536
 PRIOR FILING DATE: 1999-02-17
 PRIOR APPLICATION NUMBER: 60/124,658
 PRIOR FILING DATE: 1999-03-16
 PRIOR APPLICATION NUMBER: 09/038,261
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 09/203,939
 PRIOR FILING DATE: 1998-12-02
 PRIOR APPLICATION NUMBER: 09/251,835
 PRIOR FILING DATE: 1999-02-17
 PRIOR APPLICATION NUMBER: 09/308,503
 PRIOR FILING DATE: 1999-05-25
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 11
 LENGTH: 136
 TYPE: PRT
 ORGANISM: SCID Mice
 US-09-564-329A-11

Best Local Similarity 84.5%; Pred. No. 1.5e-44; Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
 Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
 Qy 1 EVOLQOSGAEVLVRSGASVAKLSCTAGSFGNPKDYYIHWKQRPGQLEWIGCIPDENGDTY 60
 Db 14 EVOLQOSGAEVLVRSGASVAKLSCTAGSFGNPKDYYIHWKQRPGQLEWIGCIPDENGDTY 73
 Qy 61 APNFGGRATMADTSNTAYLQLSSITSDTAVYCYGGTIPAYNGQTLVUSA 115
 Db 74 VPKFOQKATMADTSNTAYLQLSSITSDTAVYCYKG---GFWGQGTIVUSA 125

RESULT 8
 Sequence 11, Application US/09855632
 Patient No. 6790339
 GENERAL INFORMATION:
 APPLICANT: Reiter, Robert E.
 APPLICANT: Witte, Owen N.
 APPLICANT: Saffran, Douglas C.
 TITLE OF INVENTION: PSCA, PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 FILE REFERENCE: 39435.54US14
 CURRENT APPLICATION NUMBER: US/09/855,632
 CURRENT FILING DATE: 2001-05-14
 PRIOR APPLICATION NUMBER: 09/564,329
 PRIOR FILING DATE: 2000-05-03
 PRIOR APPLICATION NUMBER: 09/359,326
 PRIOR FILING DATE: 1999-07-20
 PRIOR APPLICATION NUMBER: 09/814,279
 PRIOR FILING DATE: 1997-03-10
 PRIOR APPLICATION NUMBER: 60/071,141
 PRIOR FILING DATE: 1998-01-12
 PRIOR APPLICATION NUMBER: 60/074,675
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: 60/113,230
 PRIOR FILING DATE: 1998-12-21
 PRIOR APPLICATION NUMBER: 60/120,536
 PRIOR FILING DATE: 1999-02-17
 PRIOR APPLICATION NUMBER: 60/124,658
 PRIOR FILING DATE: 1999-03-16
 PRIOR APPLICATION NUMBER: 09/038,261
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 09/203,939
 PRIOR FILING DATE: 1998-12-02
 PRIOR APPLICATION NUMBER: 09/251,835
 PRIOR FILING DATE: 1999-02-17
 PRIOR APPLICATION NUMBER: 09/308,503
 PRIOR FILING DATE: 1999-05-25
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 11
 LENGTH: 136
 TYPE: PRT
 ORGANISM: SCID Mice
 US-09-855-632-11

Query Match 82.2%; Score 507; DB 4; Length 136;
 Best Local Similarity 84.5%; Pred. No. 1.5e-44; Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
 Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
 Qy 1 EVOLQOSGAEVLVRSGASVAKLSCTAGSFGNPKDYYIHWKQRPGQLEWIGCIPDENGDTY 60
 Db 14 EVOLQOSGAEVLVRSGASVAKLSCTAGSFGNPKDYYIHWKQRPGQLEWIGCIPDENGDTY 73
 Qy 61 APNFGGRATMADTSNTAYLQLSSITSDTAVYCYGGTIPAYNGQTLVUSA 115
 Db 74 VPKFOQKATMADTSNTAYLQLSSITSDTAVYCYKG---GFWGQGTIVUSA 125

RESULT 9
 US-09-423-439-44
 Sequence 44, Application, US/09423439
 Patent No. 6339070

Query Match 82.2%; Score 507; DB 4; Length 136;
 Best Local Similarity 84.5%; Pred. No. 1.5e-44; Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
 Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

Query Match 82.2%; Score 507; DB 4; Length 136;
 US-09-963-620-11

GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles

TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423-439-26

FILING DATE: 09-May-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 6339070-1999

FILING DATE: 10-May-1997

SEQUENCE CHARACTERISTICS:

LENGTH: 642 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLogy: linear

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-423-439-26

Query Match 81.8%; Score 505; DB 3; Length 642;
Best Local Similarity 80.8%; pred. No. 1.5e-43; Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

Qy 1 EVLOQSGAELVRSGASVKSCTASGNKIDYIHWVKRQEGLWIGCIPDENGDTY 60
Db 20 EVLOQSGAELVRSGASVKSCTASGNKIDYIHWVKRQEGLWIGCIPDENGDTY 79

Qy 61 APNFORATMTADTSNTAYLQLSISLTSDTAVYTC---YGGITTFAYWQGQTIVWUSA 116
Db 80 APKFRRKATLTDASSNTAYLHLSSTSDDTAVYCYHLIVAGYLAMDYNGQGTSAVASS 139

RESULT 11
US-09-423-439-51

Sequence 51, Application US/09423439

PATENT NO. 6339070

GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESS: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423-439-26

FILING DATE: 09-May-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294

FILING DATE: 05-May-1998

APPLICATION NUMBER: GB 9709421.3

FILING DATE: 10-May-1997

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 666 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLogy: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-423-439-51

Query Match 81.8%; Score 505; DB 3; Length 666;
Best Local Similarity 80.8%; pred. No. 1.6e-43; Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVLOQSGAELVRSAGSKLUSTASGFNIKYIHWIKQRPEQGLEWICIDPENGTYY 60
 Db 20 EVLOQSGAELVRSAGSKLUSTASGFNIKYIHWIKQRPEQGLEWICIDPENGTYY 79
 QY 61 APNFOGRATMADTSNTAYLQLSLSITSDTAVYC---YGGTITPAWGOGLTVSA 116
 Db 80 APKFRGKATLTDSSNTAYLQLSLSITSDTAVYCCHVILYAGYLAMDYWGQTSVAVS 139

RESULT 12

US-08-017-570-4

; Sequence 4, Application US/08017570

; GENERAL INFORMATION:

; PATENT NO. 5472693

; APPLICANT: GOURLIE, BRIAN B

; APPLICANT: RIXON, MARK W

; APPLICANT: MEZES, PETER S

; APPLICANT: KAPLAN, DONALD A

; APPLICANT: SCHLOM, JEFFREY

; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Duane C. Ulmer

; STREET: P.O. Box 1967

; CITY: Midland

; STATE: MI

; COUNTRY: US

; ZIP: 48641-1967

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/017,570

; FILING DATE: 1993/01/16

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: ULMER, DUANE C

; REGISTRATION NUMBER: 34,941

; REFERENCE/DOCKET NUMBER: C-38,777

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (517) 636-9104

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 124 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; REFERENCE/DOCKET NUMBER: 34,941

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (517) 636-9104

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 124 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; REFERENCE/DOCKET NUMBER: 34,941

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (517) 636-9104

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 124 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: Linear

; MOLECULE TYPE: protein

; US-08-017-570-4

; Query Match 81.5%; Score 503; DB 1; Length 124;

; Best Local Similarity 80.6%; Pred. No. 3.4e-44;

; Matches 100; Conservative 4; Mismatches 12; Indels 8; Gaps 2;

; QY 1 EVLOQSGAELVRSAGSKLUSTASGFNIKYIHWIKQRPEQGLEWICIDPENGTYY 60

; Db 1 EVLOOQSGAELVRSAGSKLUSTASGFNIKYIHWIKQRPEQGLEWICIDPENGTYY 60

; QY 61 APNFOGRATMADTSNTAYLQLSLSITSDTAVYC---YGGTITPAWGOGLTV 112

; Db 61 APKFQGKATLTDSSNTAYLQLSLSITSDTAVYCCHVILYAGYLAMDYWGQTSVAVS 139

; QY 113 TVSA 116

; Db 121 AVSS 124

; RESULT 14

; PCT-US94-01709-4

; Sequence 4, Application PC/TUS9401709

; GENERAL INFORMATION:

; APPLICANT: THE DOW CHEMICAL COMPANY

; APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES

; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Duane C. Ulmer

; STREET: P.O. Box 1967

; CITY: Midland

; STATE: MI

; RESULT 13

; US-08-421-426-4

; Sequence 4, Application US/08471426

; Patent No. 5808033

```

COUNTRY: US
ZIP: 40641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MC-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01709
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: 3B,777-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-01709-4

RESULT 15
US-09-171-945-19
Sequence 19, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 19
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: humanized
Query Match 81.4%; Score 502; DB 3; Length 255;
US-09-171-945-19
Best Local Similarity 80.0%; Pred. No. 1e-43;

```

	Matches	96;	Conservative	8;	Mismatches	12;	Indels	4;	Gaps	1;
Qy	1	EVOLOGSGAELVRSVGASVLUKSLTASGPNTIYIHWKORPEQLEWIGCIPDENGDTY	60							
Db	20	EVOLOGSGAELVRSVGASVLUKSLTASGPNTIYIHWKORPEQLEWIGCIPDENGDTY	79							
Qy	61	APNFGQRATMADISNTAVIQLQSLTSEDTAVYIC---YGGTIT---PAWGQGTYLTVSA	116							
Db	80	APKFGKATMADISNTAVIQLQSLTSEDTAVYICVHVLJAGYLAAMDYGQGTSVAVSS	139							

Search completed: December 29, 2004, 18:09:10
Job time : 31.0177 BECS

THIS PAGE BLANK (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:47:08 ; Search time 18.9823 Seconds

384.304 Million cell updates/sec

Title: US-10-774-076-5

Perfect score: 576

Sequence: 1 QAVVTOESALTTSPGEGTVAL... ALWYSHHWWFQGGTKLTIVLG 110

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgpi2_6/podata/1/1aa/5A-COMB.pep:*
- 2: /cgpi2_6/podata/1/1aa/5B-COMB.pep:*
- 3: /cgpi2_6/podata/1/1aa/6A-COMB.pep:*
- 4: /cgpi2_6/podata/1/1aa/6B-COMB.pep:*
- 5: /cgpi2_6/podata/1/1aa/PCT-US-COMB.pep:*
- 6: /cgpi2_6/podata/1/1aa/backfilesl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	559	97.0	112	3 US-09-157-370-6
2	559	97.0	269	2 US-09-157-370-6
3	559	97.0	269	2 US-09-491-988-3
4	559	97.0	402	2 US-09-491-988-9
5	559	97.0	435	2 US-09-491-988-5
6	548	95.1	128	3 US-09-348-548-2
7	548	95.1	128	3 PCT-US-95-1716-2
8	530.5	92.1	109	4 US-09-865-483-7
9	528	91.7	110	1 US-09-122-546-14
10	528	91.7	110	2 US-09-764-938-14
11	528	91.7	110	3 US-09-131-052-14
12	528	91.7	110	3 US-09-131-053A-14
13	528	91.7	110	3 US-09-131-053A-14
14	520	90.3	106	2 US-09-440-354-2
15	520	90.3	105	2 US-09-463-087-2
16	517	89.8	109	2 US-09-672-345C-1.
17	517	89.8	109	3 US-09-214-095D-1.
18	513	89.1	109	2 US-09-672-345C-2
19	513	89.1	109	3 US-09-214-095D-2
20	509	88.4	115	6 5215889
21	504	87.5	109	2 US-09-672-345C-3
22	504	87.5	109	3 US-09-214-095D-3
23	504	87.5	109	3 US-09-214-095D-121
24	502	87.2	109	2 US-09-672-345C-93
25	476	82.6	109	2 US-09-672-345C-4
26	473	82.1	99	2 US-09-672-345C-91
27	82.1			
28	469			
29	462			
30	450.5			
31	428			
32	426			
33	413.5			
34	343.5			
35	329			
36	329			
37	329			
38	329			
39	316.5			
40	315			
41	309			
42	300			
43	277			
44	265.5			
45	252			
46	238.5			
47	238.5			
48	238.5			
49	238.5			
50	238.5			
51	238.5			
52	238.5			
53	238.5			
54	238.5			
55	238.5			
56	238.5			
57	238.5			
58	238.5			
59	238.5			
60	238.5			

ALIGNMENTS

RESULT 1
US-09-157-370-6
; Sequence 6, Application US/09157370A
; Patent No. 626238
; GENERAL INFORMATION:
; APPLICANT: STEINBACHER, Boris
; INVENTOR: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; FILE REFERENCE: P8341-8072
; CURRENT APPLICATION NUMBER: US/09/157-370A
; CURRENT FILING DATE: 1998-09-21
; EARLIER APPLICATION NUMBER: 08/765,179
; EARLIER FILING DATE: 1997-01-14
; EARLIER APPLICATION NUMBER: PCT/EP95/02626
; EARLIER FILING DATE: 1995-07-06
; EARLIER APPLICATION NUMBER: DBP44 25 115.7
; EARLIER FILING DATE: 1994-07-15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.

Query Match Best Local Similarity 97.0%; Score 559; DB 3; Length 112;
Sequence 6, Appli Sequence 7, Appli Sequence 8, Appli Sequence 9, Appli Sequence 10, Conservatve Matches 107; Conservative 97.3%; Pred. No. 1.3e-48; Mismatches 0; Indels 0; Gaps 0;

QY 1 QAVVTOESALTTSPGEGTVALTCGCSSTGAVITNSANWYQBKPDILFTGSLIGGTNVRCPV 60
1 QAVVTOESALTTSPGEGTVALTCGCSSTGAVITNSANWYQBKPDILFTGSLIGGTNVRCPV 60

61 PARPGSLIGDKAALTIQGTAQEDAYFCALMYSNNHWFQGGTQLTVLG 110
61 PARPGSLIGDKAALTIQGTAQEDAYFCALMYSNNHWFQGGTQLTVLG 110

ADDRESSEE: Jules E. Goldberg
STREET: 261 Madison Avenue

CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10016-2391
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/428,257A
 FILING DATE: 07/05/95
 CLASSIFICATION: 514
 INFORMATION FOR SEQ ID NO: 72:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 269 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 -08-428-257A-72

RESULT 3
 Query Match 97.0%; Score 559; DB 2; Length 269;
 Best Local Similarity 97.3%; Pred. No. 3. 6e-48;
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Patents 0; Sequence 3, Application US/08491988
 Patent No. 5973116
 GENERAL INFORMATION:
 APPLICANT: EPELENTO, AGAMEMNON A.
 APPLICANT: SPOONER, ROBERT A.
 APPLICANT: DEMARAIN, MAHENDRA
 TITLE OF INVENTION: Compounds for targeting
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MAULAY NISSEN GOLDBERG KIEL & HAND, LLP
 STREET: 261 MADISON AVENUE
 CITY: NEW YORK
 STATE: NY
 COUNTRY: USA
 ZIP: 10016-2391
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/491,988
 FILING DATE: 18-DEC-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: GOLDBERG, JULES B.
 REGISTRATION NUMBER: 24,408
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-986-4090
 TELEFAX: 212-818-9479
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 402 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 -08-491-988-9

RESULT 4
 Query Match 97.0%; Score 559; DB 2; Length 269;
 Best Local Similarity 97.3%; Pred. No. 3. 6e-48;
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Patents 0; Sequence 9, Application US/08491988
 Patent No. 5973116
 GENERAL INFORMATION:
 APPLICANT: EPELENTO, AGAMEMNON A.
 APPLICANT: SPOONER, ROBERT A.
 APPLICANT: DEMARAIN, MAHENDRA
 TITLE OF INVENTION: Compounds for targeting
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MAULAY NISSEN GOLDBERG KIEL & HAND, LLP
 STREET: 261 MADISON AVENUE
 CITY: NEW YORK
 STATE: NY
 COUNTRY: USA
 ZIP: 10016-2391
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/491,988
 FILING DATE: 18-DEC-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: GOLDBERG, JULES B.
 REGISTRATION NUMBER: 24,408
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-986-4090
 TELEFAX: 212-818-9479
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 402 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 -08-491-988-9

RESULT 5
 Query Match 97.0%; Score 559; DB 2; Length 402;
 Best Local Similarity 97.3%; Pred. No. 5. 7e-48;
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Patents 0; Sequence 7, Application US/08491988
 Patent No. 5973116
 GENERAL INFORMATION:

APPLICANT: SPOONER, ROBERT A.
 APPLICANT: DEONARIN, MAHENDRA
 TITLE OF INVENTION: Compounds for targeting
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 STREET: 261 MADISON AVENUE
 CITY: NEW YORK
 STATE: NY
 COUNTRY: USA
 ZIP: 10016-2391
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/491,988
 FILING DATE: 18-DEC-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: GOLDBERG, JULES B.
 REGISTRATION NUMBER: 24,408
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-818-9479
 TELEFAX: 212-818-4090
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 435 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-491-988-5

Query Match Similarity 97.0%; Score 559; DB 2; Length 435;
 Best local Similarity 97.3%; Pred. No. 5.9e-48; 3; Indels 0; Gaps 0;
 Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 QAVVTOESALTTSPGETVTTCRSTGAVTTSANWQKDPDHLFTGLIGGTINRPGV 60
 Db 158 QAVVTOESALTTSPGETVTTCRSTGAVTTSANWQKDPDHLFTGLIGGTINRPGV 217
 QY 61 PARFGSLIGDKAALTITGAQTEDEAIYCALWVSNHWVGEGGTKLTVLG 110
 Db 218 PARFGSLIGDKAALTITGAQTEDEAIYCALWVSNHWVGEGGTKLTVLG 267

RESULT 7
 US-08-348-548-2
 Sequence 2, Application US/08348548
 Patient No. 6258529
 GENERAL INFORMATION:
 APPLICANT: Berdoz, Jose
 APPLICANT: Krahenbuhl, Jean Pierre
 TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
 NUMBER OF SEQUENCES: 108
 CORRESPONDENCE ADDRESS:
 STREET: 225 Franklin Street, Suite 3100
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/348,548
 FILING DATE: 01-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 06132/009001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-5070
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 128 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-348-548-2

Query Match Similarity 95.1%; Score 548; DB 3; Length 128;
 Best local Similarity 96.3%; Pred. No. 1.9e-47; 0; Mismatches 4; Indels 0; Gaps 0;
 Matches 105; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/491,988
 FILING DATE: 18-DEC-1995
 CLASSIFICATION: 424

QY 1 QAVVTOESALTTSPGETVTLCRSSTGAVTTSANWVQEKPDHLFTGLGGTINRPGV 60 ; TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
Db 20 QAVVTOESALTTSPGETVTLCRSSTGAVTTSANWVQEKPDHLFTGLGGTINRPGV 79 ; FILE REFERENCE: 1559-0197P
; CURRENT APPLICATION NUMBER: US/09/865,483
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-865-483-7

RESULT 8
PCT-US95-15716-2
; Sequence 2, Application PC/PCT-US9515716

GENERAL INFORMATION:

APPLICANT: Berdoz, Jose
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT-US95/15716

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/348,548

FILING DATE: 01-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 3,0,162

TELECOMMUNICATION/DOCKET NUMBER: 06132/009001

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-5070

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 128 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-15716-2

Query Match 95.1%; Score 548; DB 5; Length 128;
Best Local Similarity 96.3%; Pred. No. 1,9e-47; Matches 105; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QAVVTOESALTTSPGETVTLCRSSTGAVTTSANWVQEKPDHLFTGLGGTINRPGV 60 ; TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
Db 20 QAVVTOESALTTSPGETVTLCRSSTGAVTTSANWVQEKPDHLFTGLGGTINRPGV 79 ; FILE REFERENCE: 1559-0197P
; CURRENT APPLICATION NUMBER: US/09/865,483
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-865-483-7

RESULT 10
US-08-122-546-14
; Sequence 14, Application US/08122546
; PATENT NO. 5591593
; GENERAL INFORMATION:
APPLICANT: Courtenay-Luck, Nigel S
TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OF PEM MUCIN
TITLE OF INVENTION: TANDEM REPEAT SPECIFIC MONOClonAL ANTIBODY
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jules E Goldberg, Esq.
STREET: 261 Madison Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/122,546

FILING DATE: 09/29/93

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Goldberg, Jules E

REGISTRATION NUMBER: 2,4,408

TELECOMMUNICATION/DOCKET NUMBER: JG-BPC-1069PCT

TELEPHONE: (212) 818-9419

TELEFAX: (212) 818-9419

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-122-546-14

Query Match 91.8%; Score 528; DB 1; Length 110;
Best Local Similarity 91.8%; Pred. No. 1.6e-45; Matches 101; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QAVVTOESALTTSPGETVTLCRSSTGAVTTSANWVQEKPDHLFTGLGGTINRPGV 60 ; TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
Db 1 QAVVTOESALTTSPGETVTLCRSSTGAVTTSANWVQEKPDHLFTGLGGTINRPGV 60 ; FILE REFERENCE: 1559-0197P
; CURRENT APPLICATION NUMBER: US/09/865,483
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-865-483-7

QY 61 PARFSGSLIGDKAALTITGAQTEDAYFALWVSNHWVFGGGKLTVLG 110.
Db 61 PARFSGSLIGDKAALTITGAQTEDAYFALWVSNHWVFGGGKLRSLG 110.

RESULT 11
US-08-764-938-14
; Sequence 14, Application US/08764938
; Patent No. 5833943
; GENERAL INFORMATION:
; APPLICANT: Courtney-Luck, Nigel S
; TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OR PEM MUCIN
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E Goldberg, Esq.
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08764,938
; FILING DATE: December 13, 1996
; CLASSIFICATION:
; REFERENCE/DOCKET NUMBER: JG-EPC-1069C-3
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 985-4090
; TELEFAX: (212) 813-9479
; INFORMATION FOR SEQ ID NO: 14:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 986-4090
; TELEX/FAX: (212) 818-9479
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-131-052-14
; Query Match, Best Local Similarity 91.7%; Score 528; DB 3; Length 110;
; Sequence 14, Application US/09131052
; Patent No. 6174691
; Matches 101; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Courtney-Luck, Nigel S
; TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OR PEM MUCIN
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E Goldberg, Esq.
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/131,053A
; FILING DATE: August 7, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REFERENCE/DOCKET NUMBER: JG-EPC-1069C-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 986-4090
; TELEX/FAX: (212) 818-9479
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

RESULT 12
US-09-131-052-14
; Sequence 14, Application US/09131052
; Patent No. 6174691
; GENERAL INFORMATION:
; APPLICANT: Courtney-Luck, Nigel S
; TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OR PEM MUCIN
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E Goldberg, Esq.
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/131,053A
; FILING DATE: August 7, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REFERENCE/DOCKET NUMBER: JG-EPC-1069C-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 986-4090
; TELEX/FAX: (212) 818-9479
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-131-053A-14

Query Match 91.7%; Score 528; DB 3; Length 110;
 Best Local Similarity 91.8%; Pred. No. 1.6e-45;
 Matches 101; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QAVVTOBSALITSPGEVVLTCRSSGAVTISNSANWQEKPDHIFTGLIGGTINRPGVY 60
 Db 1 QAVLTQBFALITSPGETVLTICRSSTGAVTISNSANWQEKPDHIFTGLIGGTINRPGVY 60
 Qy 61 PARFSSLIGKAKALTITGAQTEDEALYFCALWYSNHWWGGTKLTIV 110
 Db 61 PARFSSLIGKAKALTITGAQTEDEALYFCALWYSNHWWGGTKLTIV 110

RESULT 14

US-08-440-354-2

; Sequence 2, Application US/08440354

; Patent No. 5907034

GENERAL INFORMATION:

; APPLICANT: Boblet, Klaus

; APPLICANT: Peter

; APPLICANT: Seemann, Gerhard

TITLE OF INVENTION: A Monoclonal Antibody Against Complexed

TITLE OF INVENTION: and No. 5907034Complexed Complexing Agents for Removing Heavy

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finneghan, Henderson, Farabow, Garrett &

; ADDRESS: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patientin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/440,354

; FILING DATE:

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/013,166

; FILING DATE: 02-FEB-1993

; APPLICATION NUMBER: -US/07/664,789

; FILING DATE: 05-MAR-1991

; APPLICATION NUMBER: DE 4007079.4

; FILING DATE: 07-MAR-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Lavin Jr., Lawrence M.

; REFERENCE NUMBER: 30,768

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 106 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-463-087-2

Query Match 90.3%; Score 520; DB 2; Length 106;
 Best Local Similarity 93.3%; Pred. No. 9.6e-45;
 Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 64 FSSGLIGKAKALTITGAQTEDEALYFCALWYSNHWWGGTKLTIV 108
 Db 62 FSSGLIGKAKALTITGAQTEDEALYFCALWYSNHWWGGTKLTIV 106

Qy 65 VTOESALITSPGETVLTICRSSTGAVTISNSANWQEKPDHIFTGLIGGTINRPGVPAR 63
 Db 62 VTOESALITSPGETVLTICRSSTGAVTISNSANWQEKPDHIFTGLIGGTINRPGVPAR 61

Qy 66 FSSGLIGKAKALTITGAQTEDEALYFCALWYSNHWWGGTKLTIV 108
 Db 62 FSSGLIGKAKALTITGAQTEDEALYFCALWYSNHWWGGTKLTIV 106

Query Match 90.3%; Score 520; DB 2; Length 106;

Best Local Similarity 93.3%; Pred. No. 9.6e-45;
 Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 VTOESALITSPGETVLTICRSSTGAVTISNSANWQEKPDHIFTGLIGGTINRPGVPAR 63
 Db 2 VTOESALITSPGETVLTICRSSTGAVTISNSANWQEKPDHIFTGLIGGTINRPGVPAR 61

Search completed: December 29, 2004, 18:09:12

Job time : 20.9823 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:46:45 ; Search time: 14.677 Seconds

Sequence: 1 DIQMTQSPSLSASVGDRTV.....CQYDPRPYTRGGGTVKEIK 107
701.451 Million cell updates/sec

Title: US-10-774-076-14
Perfect score: 561

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%*

Listing first 45 summaries

Database : PIR_79;*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	86.6	127	2	S52447
2	474	84.5	128	1	KMSTI
3	470	83.8	234	2	SL4237
4	459	81.8	128	2	PL0101
5	453	80.7	129	2	S52789
6	452	80.6	125	2	S40333
7	451	80.4	108	2	B49047
8	450	80.2	132	2	S40334
9	449	80.0	129	2	S40369
10	447	79.7	123	2	S40313
11	446	79.5	106	2	S20652
12	446	79.1	108	1	KLHUAU
13	444	79.1	108	2	I39154
14	444	79.1	125	2	S40349
15	443	79.0	108	1	KLHURU
16	443	79.1	108	1	KLHURY
17	442	78.8	108	1	KVMSL6
18	442	78.8	115	1	KVMSL6
19	442	78.8	123	1	S40331
20	441	78.6	108	1	KLHUWE
21	440	78.4	108	2	S19674
22	440	78.4	125	2	S40316
23	439	78.3	107	2	I69017
24	439	78.3	108	1	KLHURE
25	439	78.3	125	2	S40353
26	439	78.3	127	2	S40367
27	438	78.1	125	2	S40350
28	436	77.7	104	2	S13700
29	77.7		117	2	S46371

ALIGNMENTS

RESULT 1
S52447
IG kappa chain v region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C;Accession: S52447

R;Bardoz, J.; Krashenbuhl, J.P.

submitted to the EMBL Data Library, November 1994

A;Description: Specific amplification by the polymerase chain reaction of rearranged ge-

A;Prediction: S52445

A;Reference number: S52447

A;Status: preliminary

A;Molecule type: DNA

A;Cross-references: EMBL:X82688; NID:9673443; PID:CAA58009.1; RID:967344

C;Genetics:

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;36-110/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 86.6%; Score 486; DB 2; Length 127;
Matches 89; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

QY

1 DIQMTQSPSLSASVGDRTV.....CQYDPRPYTRGGGTVKEIK 107

Db

21 DIKOTQSPESSMYASIGERVITICKASQDINNLYAWPQQPKPGSKPQLTILRNLIDGES 80

QY

61 RFSGSGSGDQYDTISIQSOPEDATYQIQCQYDPRPYTRGGGTVKEIK 107

Db

81 RFSGSGSGDQYSWLTISLEVDWGIYQLOFDERPYTRGGGTKEIK 127

RESULT 2

KMSTI

IG kappa chain precursor V region (RI) - mouse

C;Species: Mus musculus (house mouse)

C;Accession: A01920 #sequence_revision 08-Oct-1981 #text_change 09-Jul-2004

C;Accession: A01920 #sequence_revision 31-Dec-1980

R;Altenburger, W.; Steinmetz, M.; Zachau, H.G.

Nature 287, 603-607, 1980

A;Title: Functional and non-functional joining in immunoglobulin light chain genes of a

A;Reference number: A01920; MUID:81052342; PMID:6776411

A;Accession: A01920

A;Molecule type: mRNA

A;Residues: 1-128 <ALT>

A;Cross-references: UNIPROT:P01637; GB:VP0772; NID:951636; PID:CAA24150.1; RID:9762979

A;Note: the sequence was determined from the differentiated gene

C;Genetics:

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer

F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-128/Product: Ig kappa chain V region (T1) #status predicted <MAT>

F;43-108/Disulfide bonds: #status predicted

Query Match 84.5%; Score 474; DB 1; Length 128;

Best Local Similarity 81.3%; Pred. No. 7..6e-34; Matches 87; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTICKASODINSYLSWFOQKGKAPKLIVRANRLVDGVS 60
Db 21 DIQMTQSPSSMSASLGRVTICKASODINSYLSWFOQKGKSPKLIVRANRLVDGVS 80

Ov 61 RFGSGSGQDYLTTISLQPEDPATYCYCLODEPYTFCGGTKVEIK 107
Db 81 RFSGSGSGQEVSLTISLEEDMGIVFCYCLODEPYTFCGGTKVEIK 127

RESULT 3

S14237
Ig kappa chain precursor (15G5) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S14237
R; Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.

Bur. J. Biochem. 192, 67-77, 1990

A;Title: Construction and characterization of a recombinant murine monoclonal antibody d

A;Reference number: S14236; MUID:91006173; PMID:2209622

A;Accession: S14237
A;Molecule type: mRNA

A;Residues: 1-234 <VAN>

C;Cross-references: EMBL:X56394; NID:951622; PID:CAA39805.1; PID:951623

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin <IMM>

Query Match 83.8%; Score 470; DB 2; Length 234;

Best Local Similarity 81.3%; Pred. No. 3e-33; Matches 87; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTICKASODINSYLSWFOQKGKAPKLIVRANRLVDGVS 60
Db 21 DIQMTQSPSSMSASLGRVTICKASODINSYLSWFOQKGKSPKLIVRANRLVDGVS 80

Ov 61 RFGSGSGQDYLTTISLQPEDPATYCYCLODEPYTFCGGTKVEIK 107
Db 81 RFSGSGSGQEVSLTISLEEDMGIVFCYCLODEPYTFCGGTKVEIK 127

RESULT 4

PLO101
Ig kappa chain precursor v region (40-140) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000

C;Accession: PLO101
R;Near, R.I.; Haber, E.

Mol. Immunol. 26, 371-382, 1989

A;Title: Characterization of the heavy and light chain immunoglobulin variable region g

A;Reference number: PLO100; MUID:89238344; PMID:2497340

A;Accession: PLO101
A;Molecule type: DNA

A;Residues: 1-128 <NEA>

A;Experimental source: strain A/J

A;Note: the VK40-140 gene segment can be classified as a member of the Vk9 subgroup

C;Inttrons: 17..1
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <SIG>

RESULT 5

S52789
Ig kappa chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

R;Rocca, A.; Khamilchi, A.A.; Touchard, G.; Meugnot, B.; Ronco, P.; Denory, I.; Daret,

A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-

A;Reference number: S52789

A;Accession: S52789
A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-129 <ROC>

C;Cross-references: EMBL:X85995; NID:9759588; PID:CAA59987.1; PID:9758589

C;Keywords: heterotetramer; immunoglobulin F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 453; DB 2; Length 129;

Best Local Similarity 80.4%; Pred. No. 4..8e-32; Matches 86; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTICKASODINSYLSWFOQKGKAPKLIVRANRLVDGVS 60
Db 23 DIQMTQSPSSMSASLGRVTICKASODINSYLSWFOQKGKSPKLIVRANRLVDGVS 82

Ov 61 RFGSGSGQDYLTTISLQPEDPATYCYCLODEPYTFCGGTKVEIK 107
Db 83 RFSGSGSGQEVSLTISLEEDMGIVFCYCLODEPYTFCGGTKVEIK 129

RESULT 6

S540333
Ig kappa chain V-J region - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40333
R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3251, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-125 <KLE>

C;Cross-references: EMBL:X72443; NID:9441354; PID:CAA5111.1; PID:9441355

C;Keywords: heterotetramer; immunoglobulin F;34-108/Domain: immunoglobulin homology <IMM>

RESULT 7

F;36-110/Domain: immunoglobulin homology <IMM>

F;115-128/Domain: J segment #status predicted <JRB>

Query Match 80.6%; Score 452; DB 2; Length 125;

Best Local Similarity 78.5%; Pred. No. 5..7e-32; Matches 84; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTICKASODINSYLSWFOQKGKAPKLIVRANRLVDGVS 60

Qy	61 RFSGSGSGCDYLTISLQPEDFATYYCQDYDERPYTFCGGTKVEIK 107
Db	79 RFSGSGSGCFITLTISLQPEDFATYYCQDYDERPYTFCGGTKVEIK 125
RESULT 7	R;Griffith, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993. A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Accession: S36264 A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-107 <GR> A;Cross-references: EMBL:Z18845; NID:g33426; PIDN:CAA79297.1; PID:g939919
C;Species: Homo sapiens (man)	C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000	C;Accession: S36264
C;Accession: S36264	R;Klein, R.; Jaenichen, R.; Zachau, H.G. Bur. J. Immunol. 23, 324-327, 1993
Qy	R;J. Immunol. 23, 324-327, 1993 A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
Db	A;Accession: S40334
RESULT 8	A;Status: preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-132 <KLE> A;Cross-references: EMBL:X72444
Qy	A;Superfamily: immunoglobulin V region; immunoglobulin homology
Db	C;Keywords: heterotetramer; immunoglobulin P;16-50/Domain: immunoglobulin homology <IMM>
Query Match	80.4%; Score 451; DB 2; Length 107;
Best Local Similarity	79.4%; Pred. No. 6e-32; Mismatches 10; Indels 0; Gaps 0;
Matches	85; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
Qy	1 DIQMTQSPLSLASVGDRVTITCKASQDINSVLSWFOOKPGKAPKTLIYRANRLDGVS 60
Db	1 DIQMTQSPLSLASVGDRVTITCKASQDINSVLSWFOOKPGKAPKTLIYRANRLDGVS 60
Qy	61 RFSGSGSGCDYLTISLQPEDFATYYCQDYDERPYTFCGGTKVEIK 107
Db	61 RFSGSGSGCDYLTISLQPEDFATYYCQDYDERPYTFCGGTKVEIK 107
RESULT 9	R;Klein, R.; Jaenichen, R.; Zachau, H.G. Bur. J. Immunol. 23, 324-327, 1993 A;Title: Human monoclonal striational autoantibody STRAB SA-1A) - human (fragment B49047) A;Accession: B49047 A;Status: preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-108 <VIC> A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
C;Species: Homo sapiens (man)	C;Accession: B49047 C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047	R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Qy	Bur. J. Immunol. 22, 2231-2236, 1992
Db	A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes A;Reference number: B49047; MUID:92307224; PMID:156616
Qy	A;Accession: B49047 A;Status: preliminary A;Molecule type: nucleic acid
Db	A;Residues: 1-108 <VIC>
Qy	A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
Db	A;Experimental source: thymic B lymphocytes
Qy	A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
Db	C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;16-90/Domain: immunoglobulin homology <IMM>
Query Match	80.4%; Score 451; DB 2; Length 108;
Best Local Similarity	80.2%; Pred. No. 6e-32; Mismatches 13; Indels 0; Gaps 0;
Matches	88; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
Qy	1 DIQMTQSPLSLASVGDRVTITCKASQDINSVLSWFOOKPGKAPKTLIYRANRLDGVS 60
Db	1 DIQMTQSPLSLASVGDRVTITCKASQDINSVLSWFOOKPGKAPKTLIYRANRLDGVS 60
Qy	61 RFSGSGSGCDYLTISLQPEDFATYYCQDYDERPYTFCGGTKVEIK 107
Db	61 RFSGSGSGCDYLTISLQPEDFATYYCQDYDERPYTFCGGTKVEIK 107
RESULT 10	R;Klein, R.; Jaenichen, R.; Zachau, H.G. Bur. J. Immunol. 23, 324-327, 1993 A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
Qy	A;Accession: S40334
Db	A;Accession: S40369
Qy	61 RFSGSGSGCDYLTISLQPEDFATYYCQDYDERPYTFCGGTKVEIK 107
Db	61 RFSGSGSGCDYLTISLQPEDFATYYCQDYDERPYTFCGGTKVEIK 107
RESULT 11	R;Klein, R.; Jaenichen, R.; Zachau, H.G. Bur. J. Immunol. 23, 324-327, 1993 A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
Qy	A;Accession: S40313
Db	A;Accession: S40313
Qy	Ig kappa chain V-J region - human
Db	C;Species: Homo sapiens (man)
Qy	C;Accession: S40313
Db	R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Qy	Eur. J. Immunol. 23, 3248-3271, 1993
Db	A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40313
A;Status: preliminary; translation not shown
A;Residues: 1-123 <GL>
A;Cross-references: EMBL:X72423; NID:9441314; PID:CAA51091_1; PID:9441315
C;Superfamily: heterotetramer; immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
P;32-106/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 447; DB 2; Length 123;
Best Local Similarity 81.3%; Pred. No. 1_5e-31; Mismatches 12; Indels 0; Gaps 0;
Matches 87; Conservative 8; MisMatches 12; Indels 0; Gaps 0;

RESULT 12

1 DQMTQSPSLSASVGDRVTITCKASODINSYLSWFOOKPGKAPKTLIYRANLYDGVPS 60
Db 17 DQMTQSPSLSASVGDRVTITCKASODINSYLSWFOOKPGKAPKTLIYRANLYDGVPS 76

QY 61 RFSGSGSGGDDYTITSSLOPEDFATYYCYQDLYDEPFYRGKPKLTVKIK 107
R;Linosman, M.; Fasy, T. M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992

A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Reference number: S20639
A;Accession: S20652
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-106 <LOS>
C;Cross-references: EMBL:X65008; NID:952649; PMID:CA46141_1; PID:952650
C;Keywords: heterotetramer; immunoglobulin
P;16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 446; DB 2; Length 106;
Best Local Similarity 77.4%; Pred. No. 1.6e-31; Mismatches 9; Indels 0; Gaps 0;
Matches 82; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 DQMTQSPSLSASVGDRVTITCKASODINSYLSWFOOKPGKAPKTLIYRANLYDGVPS 60
Db 1 DQMTQSPSLSASVGDRVTITCKASODINSYLSWFOOKPGKAPKTLIYRANLYDGVPS 60

QY 61 RFSGSGSGGDDYTITSSLOPEDFATYYCYQDLYDEPFYRGKPKLTVKIK 107
Db 61 RFSGSGSGGDDYTITSSLOPEDFATYYCYQDLYDEPFYRGKPKLTVKIK 107

RESULT 13

Ig kappa chain V-I region (Au) - human
C;Species: Homo sapiens (man)
C;Accession: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
R;Schneichl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub
A;Reference number: A91653; MUID:7218944; PMID:5028201
A;Accession: A91653
A;Molecule type: protein
A;Residues: 1-108 <SCH>

A;Cross-references: UNIPROT:P01594
A;Note: the C region of this chain has the Inv (3) marker
R;Rehhammer, H.; Schiffer, M.; Bpp, O.; Colman, P.M.; Lattman, E.B.; Schwager, P.; Stei
Biology. Struct. Mech. 1, 139-146 1975
A;Title: The structure determination of the variable portion of the Bence-Jones protein
A;Reference number: A90729; MUID:7702433; PMID:234024

A;Contents: annotation; X-ray crystallography
A;Note: the structure of the V region was determined by molecular replacement methods
R;Steiner, V.; Chang, J.Y.
R;FBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances ti
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (ka
chain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
R;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 79.1%; Score 444; DB 1; Length 108;
Best Local Similarity 79.4%; Pred. No. 2.4e-31; Mismatches 7; Indels 0; Gaps 0;
Matches 85; Conservative 7; MisMatches 15; Indels 0; Gaps 0;

RESULT 14

Ig kappa chain (BRB) - human (fragment)
C;Species: Homo sapiens (man)
C;Accession: I39154
R;Schormann, N.; Murell, J.R.; Liepnies, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A;Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposal
A;Reference number: I39154; MUID:9603804; PMID:7568160
A;Accession: I39154
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-108 <RES>
A;Cross-references: EMBL:U31344; NID:944925; PID:AA79238_1; PID:944926
C;Superfamily: heterotetramer; immunoglobulin V region; immunoglobulin homology
P;16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 444; DB 2; Length 108;
Best Local Similarity 80.4%; Pred. No. 2.4e-31; Mismatches 15; Indels 0; Gaps 0;
Matches 86; Conservative 6; MisMatches 15; Indels 0; Gaps 0;

RESULT 15

Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S40349
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

THIS PAGE BLANK (use reverse)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

ON protein - protein search, using SW model

Run on: December 29, 2004, 18:05:34 ; Search time 61.8643 Seconds
(without alignments)
622.182 Million cell updates/sec

Title: US-10-774-076-14
Perfect score: 561
Sequence: 1 DIQMTQSPSSLSASVGDRTV.....CLQYDBFPYTFGGTKEIK 107

Scoring table: BLOSUM2
gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 35972771 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA,*

1: /cgtr_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
2: /cgtr_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
3: /cgtr_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: *
4: /cgtr_6/ptodata/2/pubpaa/US10_PUBCOMB.pep: *
5: /cgtr_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
6: /cgtr_6/ptodata/2/pubpaa/PCTRS_PUBCOMB.pep: *
7: /cgtr_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: *
8: /cgtr_6/ptodata/2/pubpaa/PUBCOMB.pep: *
9: /cgtr_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: *
10: /cgtr_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep: *
11: /cgtr_6/ptodata/2/pubpaa/US10_PUBCOMB.pep: *
12: /cgtr_6/ptodata/2/pubpaa/US09_NEW_PUB.pep: *
13: /cgtr_6/ptodata/2/pubpaa/US10_PUBCOMB.pep: *
14: /cgtr_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep: *
15: /cgtr_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep: *
16: /cgtr_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep: *
17: /cgtr_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: *
18: /cgtr_6/ptodata/2/pubpaa/US11_NEW_PUB.pep: *
19: /cgtr_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: *
20: /cgtr_6/ptodata/2/pubpaa/US60_PUBCOMB.pep: *

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	561	100.0	107	17 US-10-774-076-14 Sequence 14, Appl
2	561	100.0	127	17 US-10-774-076-14 Sequence 19, Appl
3	510	90.9	107	9 US-09-158-120-20 Sequence 20, Appl
4	503	89.7	107	17 US-10-774-076-3 Sequence 3, Appl
5	503	89.7	127	17 US-10-774-076-11 Sequence 11, Appl
6	502	89.5	107	14 US-10-340-189-27 Sequence 27, Appl
7	502	89.5	107	15 US-10-325-696-27 Sequence 27, Appl
8	499	88.9	107	15 US-10-462-062-107 Sequence 107, Appl
9	499	88.9	107	16 US-10-472-905b-96 Sequence 96, Appl
10	499	88.9	127	15 US-10-462-062-182 Sequence 182, Appl
11	499	88.9	127	16 US-10-472-905b-122 Sequence 122, Appl
12	498	88.8	107	14 US-10-127-890-125 Sequence 125, Appl
13	498	88.8	107	14 US-10-340-189-87 Sequence 87, Appl

RESULT 1
US-10-774-076-14
; Sequence 14, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphilargin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774-076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent version 3.2
; SEQ ID NO 14
; LENGTH: 107
; OTHER INFORMATION: Humanized antibody
; FEATURE:
; ORGANISM: Artificial
; TYPE: PRT
; OTHER INFORMATION: Humanized antibody

ALIGNMENTS

Query Match Best Local Similarity 100.0%; Score 561; DB 17; Length 107;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTV.....CLQYDBFPYTFGGTKEIK 107
Db 1 DIQMTQSPSSLSASVGDRTV.....CLQYDBFPYTFGGTKEIK 107
61 RFSGSGSGDYDTISIQPEDATYCLQYDBFPYTFGGTKEIK 107
61 RFSGSGSGDYDTISIQPEDATYCLQYDBFPYTFGGTKEIK 107

RESULT 2

US-10-774-076-19

; Sequence 19, Application US/10774076

; Publication No. US20040210040A1

; GENERAL INFORMATION:

; APPLICANT: Protein Design Labs, Inc.

; TITLE OF INVENTION: AmphiRegulin Antibodies and Their Use to Treat Cancer and

; FILE REFERENCE: 05882.0064.NPUS01

; CURRENT APPLICATION NUMBER: US/10/774,076

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 19

; LENGTH: 127

; TYPE: PRT

; ORGANISM: Artificial

; OTHER INFORMATION: Humanized antibody

; US-10-774-076-19

; Query Match

; Best Local Similarity 100.0%; Score 551; DB 17; Length 127;

; Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Qy 1 DIQMTQSPSSASAVGDRVTICKASQDINSYLSWFOQPKGKAPTKLYRANRLVGDPS 60

; Db 2 1 DIQMTQSPSSASAVGDRVTICKASQDINSYLSWFOQPKGKAPTKLYRANRLVGDPS 80

; Qy 61 RFSGSGSGQDYLTISLQPEDFATYYCQYDRFPYFGGGTKEIK 107

; Db 81 RFSGSGSGQDYLTISLQPEDFATYYCQYDRFPYFGGGTKEIK 127

; RESULT 3

; US-10-158-120A-20

; Sequence 20, Application US/09158120A

; PATENT NO. US20020102257A1

; GENERAL INFORMATION:

; APPLICANT: JOHNSON, L.

; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GIFFILLAN, CECCHI,

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER SYSTEM: Windows95

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/158 120A

; FILING DATE: September 21, 1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/290,592

; FILING DATE: August 15, 1994

; APPLICATION NUMBER: 07/813,372

; FILING DATE: December 23, 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Olstein, Elliot M.

; REGISTRATION NUMBER: 24,025

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 973-994-1700

; FAX: 973-994-1744

; INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 AMINO ACIDS

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

; US-10-774-076-20

; Query Match

; Best Local Similarity 89.9%; Score 510; DB 9; Length 107;

; Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

; Qy 1 DIQMTQSPSSASAVGDRVTICKASQDINSYLSWFOQPKGKAPTKLYRANRLVGDPS 60

; Db 1 DIQMTQSPSTISASAVGDRVTICKASQDINSYLSWFOQPKGKAPTKLYRANRLVGDPS 60

; Qy 61 RFSGSGSGQDYLTISLQPEDFATYYCQYDRFPYFGGGTKEIK 107

; Db 61 RFSGSGSGQDYLTISLQPEDFATYYCQYDRFPYFGGGTKEIK 107

; RESULT 4

; US-10-774-076-3

; Sequence 3, Application US/10774076

; Publication No. US20040210040A1

; GENERAL INFORMATION:

; APPLICANT: Protein Design Labs, Inc.

; TITLE OF INVENTION: AmphiRegulin Antibodies and Their Use to Treat Cancer and

; FILE REFERENCE: 05882.0064.NPUS01

; CURRENT APPLICATION NUMBER: US/10/774,076

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3

; LENGTH: 107

; TYPE: PRT

; ORGANISM: mus sp.

; US-10-774-076-3

; Query Match

; Best Local Similarity 87.9%; Score 503; DB 17; Length 107;

; Matches 94; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

; Qy 1 DIQMTQSPSSASAVGDRVTICKASQDINSYLSWFOQPKGKAPTKLYRANRLVGDPS 60

; Db 1 DIQMTQSPSSMAYSLQGRVTICKASQDINSYLSWFOQPKGKAPTKLYRANRLVGDPS 60

; Qy 61 RFSGSGSGQDYLTISLQPEDFATYYCQYDRFPYFGGGTKEIK 107

; Db 61 RFSGSGSGQDYLTISLQPEDFATYYCQYDRFPYFGGGTKEIK 107

; RESULT 5

; US-10-774-076-11

; Sequence 11, Application US/10774076

; Publication No. US20040210040A1

; GENERAL INFORMATION:

; APPLICANT: Protein Design Labs, Inc.

; APPLICANT: Landolfi, et al.

; TITLE OF INVENTION: AmphiRegulin Antibodies and Their Use to Treat Cancer and

; FILE REFERENCE: 05882.0064.NPUS01

; CURRENT APPLICATION NUMBER: US/10/774,076

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 11

; LENGTH: 127

; TYPE: PRT

; ORGANISM: mmu sp.

; US-10-774-076-11

Query Match 89.7%; Score 503; DB 17; Length 127;
 Best Local Similarity 87.9%; Pred. No. 1.7e-35;
 Matches 94; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

RESULT 6
 US-10-340-189-27
 Sequence 27, Application US/10340189
 Publication No. US20030229207A1
 ; GENERAL INFORMATION:
 APPLICANT: Studnicka, Gary M.
 TITLE OF INVENTION: Modified Antibody Variable Domains
 NUMBER OF SEQUENCES: 89
 NUMBER OF SEQUENCES: 67
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 W. Madison Street, 34th Floor
 CITY: Chicago
 STATE: Illinois
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/340,189
 FILING DATE: 10-Jan-2003
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/245,202A
 FILING DATE: <Unknown>
 APPLICATION NUMBER: 08/082,842
 FILING DATE: 23-JUN-1993
 APPLICATION NUMBER: PCT/US92/10906
 FILING DATE: 14-DEC-1992
 APPLICATION NUMBER: US 07/808,464
 FILING DATE: 07-Nov-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE DOCKET NUMBER: 11023US07 / 200-71.P2.C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-9155
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 ; US-10-340-189-27

Query Match 89.5%; Score 502; DB 14; Length 107;
 Best Local Similarity 88.8%; Pred. No. 1.8e-35;
 Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

RESULT 8
 US-10-325-595-27
 Sequence 27, Application US/10325695
 Publication No. US20040005630A1
 ; GENERAL INFORMATION:
 APPLICANT: Studnicka, Gary M.
 TITLE OF INVENTION: Modified Antibody Variable Domains
 NUMBER OF SEQUENCES: 67
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th Floor
 CITY: Chicago
 STATE: IL
 COUNTRY: United States of America
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0., Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/325,696
 FILING DATE: 18-Dec-2002
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/097,980
 FILING DATE: 16-JUN-1998
 APPLICATION NUMBER: 08/107,669
 FILING DATE: 13-AUG-1993
 APPLICATION NUMBER: PCT/US92/10906
 FILING DATE: 14-DEC-1992
 APPLICATION NUMBER: US 07/808,464
 FILING DATE: 13-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Janet M. McNicholas, Ph. D.
 REGISTRATION NUMBER: 32,918
 REFERENCE DOCKET NUMBER: 11023US06/200-71.P1.C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEX: 312/707-0500
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 ; US-10-325-595-27

Query Match 89.5%; Score 502; DB 15; Length 107;
 Best Local Similarity 88.8%; Pred. No. 1.8e-35;
 Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

RESULT 9
 US-10-462-062-107
 Sequence 107, Application US/10462062
 Publication No. US20040044187A1
 ; GENERAL INFORMATION:
 APPLICANT: SATO, KOH
 ; APPLICANT: ADACHI, HIDEKI
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)

Query Match 89.5%; Score 502; DB 14; Length 107;
 Best Local Similarity 88.8%; Pred. No. 1.8e-35;
 Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

RESULT 10
 US-10-462-062-107
 Sequence 107, Application US/10462062
 Publication No. US20040044187A1
 ; GENERAL INFORMATION:
 APPLICANT: SATO, KOH
 ; APPLICANT: ADACHI, HIDEKI
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)

Query Match 89.5%; Score 502; DB 15; Length 107;
 Best Local Similarity 88.8%; Pred. No. 1.8e-35;
 Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

RESULT 11
 US-10-462-062-107
 Sequence 107, Application US/10462062
 Publication No. US20040044187A1
 ; GENERAL INFORMATION:
 APPLICANT: SATO, KOH
 ; APPLICANT: ADACHI, HIDEKI
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)

TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES

FILE REFERENCE: 053466-0360

CURRENT APPLICATION NUMBER: US/10/462,062

CURRENT FILING DATE: 2003-06-16

PRIOR APPLICATION NUMBER: PCT/JP99/01768

PRIOR FILING DATE: 1999-04-02

PRIOR FILING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 183

SEQ ID NO: PatentIn Ver. 2.1

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence

US-10-462-052-107

Query Match Best Local Similarity 88.9%; Score 499; DB 15; Length 107;

Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVITCKASQDINSYLSWFOQKKGAKPVLIVRANLVDGVS

DB 1 DIQMTQSPSSLSASVGDRVITCKASQDINSYLSWFOQKKGAKPVLIVRANLVDGVS

QY 61 RFSGSGSGQDYLTISLQPEDPATYYCLODEPYTTEGSGTKVEIK 107

DB 61 RFSGSGSGTGYTISLQPEDPATYYCLODEPYTTEGSGTKVEIK 107

RESULT 9

US-10-472-905A-96

Sequence 96, Application US/10472905A

GENERAL INFORMATION:

APPLICANT: SUZUKI, KOJI

TITLE OF INVENTION: BLOOD RHEOLOGY-IMPROVING AGENT

FILE REFERENCE: 053466-0368

CURRENT APPLICATION NUMBER: US/10/472,905A

CURRENT FILING DATE: 2003-09-25

PRIOR APPLICATION NUMBER: PCT/JP02/02933

PRIOR FILING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: JP 2001-088387

NUMBER OF SEQ ID NOS: 123

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO: 96

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: amino acid sequence of version "b1" of humanized L

US-10-472-905A-96

Query Match Best Local Similarity 88.9%; Score 499; DB 16; Length 107;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRVITCKASQDINSYLSWFOQKKGAKPVLIVRANLVDGVS
1 DIQMTQSPSSLSASVGDRVITCKASQDINSYLSWFOQKKGAKPVLIVRANLVDGVS
QY 61 RFSGSGSGQDYLTISLQPEDPATYYCLODEPYTTEGSGTKVEIK 107
DB 61 RFSGSGSGTGYTISLQPEDPATYYCLODEPYTTEGSGTKVEIK 107

RESULT 10

US-10-462-062-182

Query Match Best Local Similarity 88.9%; Score 499; DB 15; Length 127;

Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVITCKASQDINSYLSWFOQKKGAKPVLIVRANLVDGVS

DB 21 DIQMTQSPSSLSASVGDRVITCKASQDINSYLSWFOQKKGAKPVLIVRANLVDGVS

QY 61 RFSGSGSGQDYLTISLQPEDPATYYCLODEPYTTEGSGTKVEIK 107

DB 81 RFSGSGSGTGYTISLQPEDPATYYCLODEPYTTEGSGTKVEIK 127

US-10-472-905A-122

Query Match Best Local Similarity 88.9%; Score 499; DB 15; Length 127;

Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVITCKASQDINSYLSWFOQKKGAKPVLIVRANLVDGVS

DB 21 DIQMTQSPSSLSASVGDRVITCKASQDINSYLSWFOQKKGAKPVLIVRANLVDGVS

QY 61 RFSGSGSGQDYLTISLQPEDPATYYCLODEPYTTEGSGTKVEIK 107

DB 21 DIQMTQSPSSLSASVGDRVITCKASQDINSYLSWFOQKKGAKPVLIVRANLVDGVS

QY 61 RFSGSGSGQDYLTISLQPEDPATYYCLODEPYTTEGSGTKVEIK 107

Db 81 RPSSGSGTGTLYTISLQPEDATYCYCLOHGESPYTEGGTKVEIK 127

RESULT 12
US-10-127-890-125

Sequence 125, Application US/10127890
Publication No. US20030166196A1

GENERAL INFORMATION:
APPLICANT: Better, Marc D.

Carroll, Stephen F.
Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 W. Madison Street, 34th floor
CITY: Chicago
STATE: Illinois

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127-890

FILING DATE: 23-APR-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/645,360

FILING DATE: 13-MAY-1996
CLASSIFICATION: 530

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994
CLASSIFICATION: 530

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993
CLASSIFICATION: 530

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992
CLASSIFICATION: 530

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992
CLASSIFICATION: 530

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70-P4

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889

TELEX: 650 388-1248
TELEFAX: 312/707-9155

INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids

SEQUENCE DESCRIPTION: SEQ ID NO: 125:
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 125:
US-10-127-890-125

Query Match 88.8%; Score 498; DB 14; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.9e-35; Indels 0; Gaps 0;
Matches 96; Conservative 3; Mismatches 8;

Query Match 88.8%; Score 498; DB 14; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.9e-35; Indels 0; Gaps 0;
Matches 96; Conservative 3; Mismatches 8;

1 DIQMOSPSLSSASVGDRITTCRASODINISLWSWQPKRGKAKTLYRANRLVDGFS 60

1 DIQMOSPSLSSASVGDRITTCRASODINISLWSWQPKRGKAKTLYRANRLVDGFS 60

61 RPSSGSGTGTLYTISLQPEDATYCYCLOHGESPYTEGGTKVEIK 107

61 RFGSGSGTGTLYTISLQPEDATYCYCLOHGESPYTEGGTKVEIK 107

RESULT 13
US-10-340-189-87

; Sequence 87, Application US/10340189
; Publication No. US20030222207A1

GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.

TITLE OF INVENTION: Modified Antibody Variable Domains

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 W. Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois

COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/340,189

FILING DATE: 10-JAN-2003
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/245,202A

FILING DATE: <Unknown>
APPLICATION NUMBER: 08/082,842

FILING DATE: 23-JUN-1993
APPLICATION NUMBER: PCT/US92/10906

FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464

FILING DATE: 13-DEC-1991
APPLICATION NUMBER: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155

INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids

SEQUENCE DESCRIPTION: SEQ ID NO: 87:
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-10-340-189-87

Query Match 88.8%; Score 498; DB 14; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.9e-35; Indels 0; Gaps 0;
Matches 96; Conservative 3; Mismatches 8;

1 DIQMOSPSLSSASVGDRITTCRASODINISLWSWQPKRGKAKTLYRANRLVDGFS 60

1 DIQMOSPSLSSASVGDRITTCRASODINISLWSWQPKRGKAKTLYRANRLVDGFS 60

61 RPSSGSGTGTLYTISLQPEDATYCYCLOHGESPYTEGGTKVEIK 107

61 RFGSGSGTGTLYTISLQPEDATYCYCLOHGESPYTEGGTKVEIK 107

US-10-325-696-65

; Sequence 65, Application US/0325696

Publication No. US2004005630A1

GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.

TITLE OF INVENTION: Modified Antibody Variable Domains

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: IL
COUNTRY: United States of America

ZIP: 60661-1
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/325,696
FILING DATE: 18-Dec-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/097,980
FILING DATE: 16-JUN-1998
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464

FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet M. McNicholas, Ph.D.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEX/FAX: 312/707-9050

INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:

US-10-325-696-65

Query Match 88.4%; Score 496; DB 15; Length 107;
Best Local Similarity 86.0%; Pred. No. 5 7e-35;
Matches 92; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFOOKPGRKPKTLIYRANLVGVPs 60
Db 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFOOKPGRKPKTLIYRANLVGVPs 60

Qy 61 RFGSGSGQDYLTISLQPEDPATVCLQDEBPFYFGGGTKEIK 107
Db 61 RFGSGSGQDYLTISLQPEDPATVCLQDEBPFYFGGGTKEIK 107

US-10-436-782-33

Search completed: December 29, 2004, 18:42:01
Job time : 62.8643 secs

RESULT 15
US-10-436-782-33
Sequence 33 Application US/10436782
; Sequence 33 Application US/10436782
; Publication No. US20040028685A1
; GENERAL INFORMATION:
; APPLICANT: Kirch, Michael
; APPLICANT: Carles-Kinch, Kelly
; APPLICANT: Kleiner, Peter
; APPLICANT: Langermann, Solomon
; TITLE OF INVENTION: EphA2 Monoclonal Antibodies and Methods of Use Thereof
; FILE REFERENCE: 10271-097
; CURRENT APPLICATION NUMBER: US/10/436,782
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,322
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/418,213
; PRIOR FILING DATE: 2002-10-14
; PRIOR APPLICATION NUMBER: 60/418,213
; PRIOR FILING DATE: 2003-04-03

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:37:57 ; Search time 73.5428 Seconds
 521.928 Million cell updates/sec

Title: US-10-774-076-14

Perfect score: 561

Sequence: 1 DIQMTSPSSLSASAVDRT.....CLQYDEPPYTFGGSTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqb, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 listing first 45 summaries

Database : A_GeneSeq_23Sep04:
 1: geneSeqDp19808:/*
 2: geneSeqDp19903:/*
 3: geneSeqDp20005:/*
 4: geneSeqDp20018:/*
 5: geneSeqDp20024:/*
 6: geneSeqDp20038:/*
 7: geneSeqDp20039:/*
 8: geneSeqDp20048:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	RESULT	1
1	520	92.7	107 2	AAW23953	ID	AAW23953
2	520	92.7	240 2	AAW23954	XX	
3	514	91.6	107 6	ABG74710	AC	AAW23953;
4	514	91.6	107 7	ABR83157	XX	
5	514	91.6	214 6	ABG74711	DT	17-OCT-2003 (revised)
6	514	91.6	214 7	ABR83150	DT	17-JUN-1998 (first entry)
7	510	90.9	107 2	AAR92082	XX	Chimeric humanised Mus musculus A717 antibody heavy chain; variable region; diabetes; prophylactic treatment.
8	510	90.9	107 5	ABG31429	XX	KW
9	510	90.9	129 2	AAR57482	XX	Chimeric; humanised; human; murine; A717; antibody; heavy chain; variable region; diabetes; prophylactic treatment.
10	510	90.9	129 5	AAR92085	XX	Mus musculus.
11	510	90.9	129 5	AAR57482	OS	Homo sapiens.
12	502	89.5	107 2	AAW31444	OS	Chimeric.
13	502	89.5	107 8	ADL01168	OS	
14	499	88.9	107 2	AAW52124	XX	
15	499	88.9	107 4	ABY74985	PR	26-JUN-1997; 97WO-US011605.
16	499	88.9	127 6	AAO16815	XX	27-JUN-1996; 96US-00672176.
17	498	88.8	107 2	AAW41283	(EXOC-) EXOCBL INC.	
18	498	88.8	107 8	AAW58515	PI	Cohen MP, Shearman CW;
19	498	88.8	107 8	ADL01228	XX	
20	496	88.4	107 8	ADB85729	DR	WPI; 1998-076916/07.
21	496	88.4	107 8	ADL22067	DR	N-PSDB; AA0V0637.
22	494	88.1	237 7	ADB57549	XX	
23	494	88.1	237 7	ADD47098	PT	New humanised antibodies specific for glycated albumin - prepared by recombinant expression of humanised mouse antibodies, useful for, e.g. treating diabetic vasculopathy.
24	494	88.1	237 7	ADD48668	PT	Example 2; Page 15; 27pp; English.
25	494	88.1	246 4	AAW86037	XX	The sequence is that of a humanised variable region of the A717 antibody light chain VI-1. The antibody has specificity for glycated albumin (GA) and is capable of neutralising the effects of GA in vivo. It can be used in the manufacture of therapeutics useful for the prophylactic treatment of complications of diabetes (especially diabetic vasculopathy and retinopathy) and atherosclerotic cardiovascular disease. The genetically engineered antibodies are specific as they only interact with GA but not other proteins and may be easily prepared in pure form. (updated on 17-OCT-2003 to standardise OS field)

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description	RESULT	1
1	520	92.7	107 2	AAW23953	ID	AAW23953
2	520	92.7	240 2	AAW23954	XX	
3	514	91.6	107 6	ABG74710	AC	AAW23953;
4	514	91.6	107 7	ABR83157	XX	
5	514	91.6	214 6	ABG74711	DT	17-OCT-2003 (revised)
6	514	91.6	214 7	ABR83150	DT	17-JUN-1998 (first entry)
7	510	90.9	107 2	AAR92082	XX	Chimeric humanised Mus musculus A717 antibody heavy chain; variable region; diabetes; prophylactic treatment.
8	510	90.9	107 5	ABG31429	XX	KW
9	510	90.9	129 2	AAR57482	XX	Chimeric; humanised; human; murine; A717; antibody; heavy chain; variable region; diabetes; prophylactic treatment.
10	510	90.9	129 5	AAR92085	XX	Mus musculus.
11	510	90.9	129 5	AAR57482	OS	Homo sapiens.
12	502	89.5	107 2	AAW31444	OS	Chimeric.
13	502	89.5	107 8	ADL01168	OS	
14	499	88.9	107 2	AAW52124	XX	
15	499	88.9	107 4	ABY74985	PR	26-JUN-1997; 97WO-US011605.
16	499	88.9	127 6	AAO16815	XX	27-JUN-1996; 96US-00672176.
17	498	88.8	107 2	AAW41283	(EXOC-) EXOCBL INC.	
18	498	88.8	107 8	AAW58515	PI	Cohen MP, Shearman CW;
19	498	88.8	107 8	ADL01228	XX	
20	496	88.4	107 8	ADB85729	DR	WPI; 1998-076916/07.
21	496	88.4	107 8	ADL22067	DR	N-PSDB; AA0V0637.
22	494	88.1	237 7	ADB57549	XX	
23	494	88.1	237 7	ADD47098	PT	New humanised antibodies specific for glycated albumin - prepared by recombinant expression of humanised mouse antibodies, useful for, e.g. treating diabetic vasculopathy.
24	494	88.1	237 7	ADD48668	PT	Example 2; Page 15; 27pp; English.
25	494	88.1	246 4	AAW86037	XX	The sequence is that of a humanised variable region of the A717 antibody light chain VI-1. The antibody has specificity for glycated albumin (GA) and is capable of neutralising the effects of GA in vivo. It can be used in the manufacture of therapeutics useful for the prophylactic treatment of complications of diabetes (especially diabetic vasculopathy and retinopathy) and atherosclerotic cardiovascular disease. The genetically engineered antibodies are specific as they only interact with GA but not other proteins and may be easily prepared in pure form. (updated on 17-OCT-2003 to standardise OS field)

Sequence 107 AA;	
Query Match	92.7%; Score 520; DB 2; Length 107;
Best Local Similarity	92.5%; Pred. No. 8; 5e-33;
Matches	Mismatches 4; Indels 0; Gaps 0;
99; Conservative	
Oy	1 DIQMTQSPLSASVGRVTICKASQDINSVSWFOOKPGKAPKILYRANKLVDAPS 60
Db	1 DIQMTQPSLSSASVGRVTICKASQDISTSLSWFOOKPGKAPKISLYHTRLLGCVPS 60
Oy	61 RFGSGSAGQDYITLTISSLOPEDPATYCYLQDNPYPVTPGGGTKEIK 107
Db	61 RFGSGSAGTDFITLSSLOPEDPATYCYLQDNPYPVTPGGGTKEIK 107
RESULT 2	
AAW23954	
ID AAW23954	standard; protein; 240 AA.
XX	
XX	
AC	
XX	
DT 17-OCT-2003	(revised)
DT 17-JUN-1998	(first entry)
DE Chimeric humanised Mus musculus A717 antibody ScFv.	
KW Chimeric; humanised; human; murine; A717; antibody; ScFv;	
variable region; diabetes; prophylactic treatment.	
XX	
OS Mus musculus.	
OS Homo sapiens.	
OS ChimERIC.	
PN WO974429-A1.	
XX	
DD 31-DEC-1997.	
CX 26-JUN-1997;	97WO-US011605.
CX 27-JUN-1996;	96US 00672176.
EXOC- EXOCELL INC.	
I (EXOC-) EXOCELL INC.	
X Cohen MP, Shearman CW;	
X WPI; 1998-076316/07.	
X N-PSDB; AAV04638.	
New humanised antibodies specific for glycated albumin - prepared by recombinant expression of humanised mouse antibodies, useful for, e.g. treating diabetic vasculopathy.	
Example 3; Page 15-16; 27pp; English.	
The sequence is that of a humanised variable region of the A717 antibody ScFv, huA717-ScFv. The antibody has specificity for glycated albumin (GA) and is capable of neutralising the effects of GA in vivo. It can be used in the manufacture of therapeutics useful for the prophylactic treatment of complications of diabetes (especially diabetic vasculopathy and retinopathy) and atherosclerotic cardiovascular disease. The genetically engineered antibodies are specific as they only interact with GA but not other proteins and may be easily prepared in pure form. (Updated on 17-Oct-2003 to standardise OS field)	
Sequence 240 AA;	

RESULT	3
ABG74710	134 DINTQSSSLASVGRVITCKASQDIDSYLSWFOOKPGKAKPSLIVHTNRLDGVPs 193
ID	ABG74710 standard; protein, 107 AA.
AC	ACG74710;
XX	
DT	10-MAY-2003 (first entry)
DB	Murine humanised Mu007 light chain variable region.
XX	KW
XX	Murine, light chain, variable region; antibody, Crohn's disease;
XX	human interleukin (IL)-1beta; antiarthritic; antiarthritic; humanised;
XX	antiinflammatory; osteopathic; antiallergic; cerebroprotective;
XX	antiasthmatic; immunosuppressive; antibacterial; vaccine; Mu007;
XX	rheumatoid arthritis; osteoarthritis; cartilage destruction; allergy;
XX	septic shock; endotoxic shock; septicemia; stroke; asthma;
OS	graft versus host disease; inflammatory bowel disease.
OS	Mus musculus.
OS	Synthetic.
XX	
PN	WO2003010282-A2.
XX	
PD	06-FEB-2003.
XX	
PF	18-JUL-2002; 2002WO-US021281.
XX	
PR	26-JUL-2001; 2001US-0307973P.
XX	14-AUG-2001; 2001US-0312278P.
PA	(ELI) LILLY & CO EUI.
XX	
PI	Bright SW, Jia AY, Kuhntoss SA, Manetta JV, Tsuruhita N;
PI	Vasquez MJ;
XX	
DR	WPI; 2003-248069/24.
DR	N-FSDB; ABQ77443.
XX	
PT	New IL-1beta antibodies, useful for treating allergy, septic or endotoxic
PT	shock, septicemia, stroke, asthma, graft versus host disease, Crohn's
PT	disease, or inflammatory bowel disease.
XX	
PS	Disclosure; Page 70-71; 98pp; English.
XX	
CC	This invention describes a novel antibody that specifically binds mature
CC	human interleukin (IL)-1beta, and binds the same epitope on mature human
CC	IL-1beta as mouse monoclonal antibody Mu007 or humanized antibody Hu007.
CC	The antibody of the invention have anti rheumatic, antiarthritic,
CC	antiinflammatory, osteopathic, antiallergic, cerebroprotective,
CC	antiasthmatic, immunosuppressive and antibacterial activity and can be
CC	used in a vaccine. The antibody is useful for manufacturing a medicament
CC	for treating rheumatoid arthritis or osteoarthritis, or for inhibiting
CC	cartilage destruction in a subject. The antibody is also useful for
CC	treating allergy, septic or endotoxic shock, septicemia, stroke, asthma,
CC	graft versus host disease, Crohn's disease, or inflammatory bowel
CC	disease. This host sequence represents the humanised murine Mu007 light chain
variable region described in the disclosure of the invention	
Sequence	107 AA;

XX	Hu007 antibody analogue light chain sequence.	FT	Region	24..34		
XX	/ analogue; humanized antibody; IL-1beta; interleukin-1 beta;	FT	/Label= CDR1			
KW	complementarity determining region; osteopathic; antiarthritic;	FT	50..56			
KW	gene therapy; CDR.	FT	/Label= CDR2			
XX	Synthetic.	FT	89..97			
OS		XX	/Label= CDR3			
XX		PN				
PN	WO2003073982-A2.	XX				
XX		PD				
PD	12-SEP-2-2003.	XX				
XX		PR				
PR	20-FEB-2-2003; 2003WO-US003117.	XX				
XX		PR				
XX	28-FEB-2-2002; 2002US-0361423P.	XX				
PA	(ELIL) LILLY & CO ELI.	PA				
XX		PI				
PT	Beals JM, Huang L, Lu J, Rogers DP, Witcher DR,	XX				
XX		DR				
DR	WPI; 2003-731644/69.	XX				
DR	N-PSDB; ACR57835.	XX				
PT	New analog of humanized antibody Hu007 that specifically binds mature IL-	PT				
PT	1 beta, useful for the manufacture of a medicament for treating	PT				
PT	rheumatoid arthritis or osteoarthritis.	XX				
XX	Claim 17; Page 13-14; 120pp; English.	PS				
PS	The invention relates to an analogue of humanized antibody Hu007 that	CC				
CC	specifically binds mature IL-beta and comprises at least one amino acid	CC				
CC	substitution at positions 54, 55 or 56 of the heavy chain complementarity	CC				
CC	determining region 2 (CDR2). The analogue is useful for the manufacture	CC				
CC	of a medicament for treating rheumatoid arthritis or osteoarthritis or	CC				
CC	for inhibiting cartilage destruction. The present sequence represents an	CC				
CC	antibody Hu007 analogue light chain sequence.	XX				
XX	Sequence 214 AA;	SQ				
Query Match	91.6%; Score 514; DB 7; Length 214;	Query Match	91.6%; Score 514; DB 7; Length 214;	FT	Region	24..34
Best Local Similarity	91.6%; Pred. No. 4.8e-32;	Best Local Similarity	91.6%; Pred. No. 4.8e-32;	FT	/Label= CDR1	
Matches	98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	Matches	98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	FT	Region	50..56
OY	1 DIQMTOSSPLSASVGDRVITICKASODINISYLWSFOQKRGKAPKTLIYRANLVDGVS 60	OY	1 DIQMTOSSPLSASVGDRVITICKASODINISYLWSFOQKRGKAPKTLIYRANLVDGVS 60	FT	/Label= CDR2	
Db	1 DIOMTQSPSPLSASVGDRVITICKASODINRVLVQPKGAKPSLILYRVRKLVDGVS 60	Db	1 DIOMTQSPSPLSASVGDRVITICKASODINRVLVQPKGAKPSLILYRVRKLVDGVS 60	FT	/Label= CDR3	
OY	61 RFSGGSGQDYLTISLQPEDFATYCKQYDERPYTGGTKVEIK 107	OY	61 RFSGGSGQDYLTISLQPEDFATYCKQYDERPYTGGTKVEIK 107	XX		
Db	61 RFSGSASGTYTTLISSLQPEDFATYCYCQDFEPYTFGGTKVEIK 107	Db	61 RFSGSASGTYTTLISSLQPEDFATYCYCQDFEPYTFGGTKVEIK 107	XX		
RESULT 7		RESULT 8				
AAR92082		ABG31429				
ID		ID				
XX	ABR92082 standard; protein; 107 AA.	XX				
AC		AC				
XX		ABG31429;				
AAR92082;		XX				
DT	16-OCT-2003 (revised)	DT	29-NOV-2002 (first entry)			
DT	15-MAY-1996 (first entry)	DE	Humanised CDR-grafted anti-RSV F glycoprotein VL #1.			
XX	Murine 1308F VL CDR-grafted K102 VL.	XX	Human-murine chimeric antibody; humanised antibody; CDR; complementarity determining region; variable heavy chain; VH; variable light chain; VL; monoclonal antibody; Mab; RSV infection; respiratory syncytial virus infection; mutant; mutagen.			
KW	Humanised antibody; chimeric antibody; antibody engineering; monoclonal antibody; Mab 1308F; respiratory syncytial virus; RSV; light chain; complementarity determining region; CDR.	KW	K102; anti-RSV F glycoprotein VL; mutant; mutagen.			
XX	Homo; sapiens.	XX	Human; Homo sapiens.			
OS	Mus musculus.	OS	Mus ap.			
OS	Chimeric.	OS	Synthetic.			
XX		XX	Chimeric.			
FH		PN	US2002102257-A1.			
Key	Location/qualifiers					

PA (MEDI-) MEDIMMUNE INC.
 XX PT
 PI Johnson LS;
 XX XX
 DR WPT; 1996-139646/14.
 DR N-PSDB; AATI6181.
 XX XX
 PT New chimeric antibodies against respiratory syncytial virus - comprise
 PT human antibodies with CDR's from the variable heavy and light chains of a
 PT murine antibody.
 XX XX
 PS Example 2; Fig 4A-4B; 55pp; English.
 XX A human-mouse chimeric antibody light chain has a human HV3 framework
 contg. complementarity determining regions (CDRs) from the variable light
 (VL) chain of murine monoclonal antibody (Mab) 1308F active against
 respiratory syncytial virus (RSV) glycoprotein F antigenic site C. DNA
 (ARK92085), was synthesized using overlapping oligonucleotides. The
 construct was used with Hui1308 VH (see ARK92084) for prodn. in COS-1
 transfectants of humanised antibody useful for treatment of RSV infection
 CC SQ Sequence 129 AA:
 CC Query Match 90.9%; Score 510; DB 2; Length 129;
 CC Best Local Similarity 88.8%; Pred. No. 6e-32; Mismatches 8; Indels 0; Gaps 0;
 CC Matches 95; Conservative 8; Mismatches 4;
 CC AC
 QY 1 DIQMTQSPSSLASAVGDRVITICKASQDINISLYSLWQOKQAKPILIVRANLVDGVPS 60
 CC Db 23 DIQMTQSPSTLUSASVGDRTTICKASQDINISLYSLWQOKQAKPILIVRANLVDGVPS 82
 CC QY 61 RRSGGSSGQDYVLTISLSQLPDDPATVYCLQDDEFPYTFGGTKVIEK 107
 CC Db 83 RPSSGSGSGTERTLTISLSQLPDDPATVYCLQDDEFPYTFGGTKVIEK 129
 RESULT 11
 ABG1444
 ID ABG31444 standard; protein; 129 AA.
 XX AC
 AC ABG31444;
 XX DT 29-NOV-2002 (first entry)
 DE Amino acid sequence for humanised antibody Hui1308VL.
 XX KW Human-murine chimeric antibody; humanised antibody; CDR;
 KW complementarity determining region; variable heavy chain; VH;
 KW variable light chain; VL; monoclonal antibody; Mab; RSV infection;
 KW respiratory syncytial virus infection; virucide; Hui1308VL; mutant;
 KW mutein.
 XX OS Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 OS Chimeric.
 XX US2002102257-A1.
 XX PD 01-AUG-2002.
 XX PF 21-SEP-1998; 98US-00158120.
 XX PR 21-SEP-1998; 98US-00158120.
 XX PA (JOHN/) JOHNSON L S.
 XX PD
 XX PF
 XX PR
 XX PA
 XX PT
 XX PT
 XX PR
 XX DR
 XX XX
 PT New human-murine chimeric antibody useful for preventing or treating
 PT respiratory syncytial viral (RSV) infection, contains at least one
 PT complementarity determining region from a murine antibody.
 XX PS
 XX Example 2; Fig 4; 33pp; English.
 CC The present invention relates to a human-murine chimeric antibody
 CC comprising a human antibody containing at least one complementarity
 CC determining region (CDR) from each of the variable heavy (VH) and
 CC variable light (VL) chains of a non-human, preferably murine, monoclonal
 CC antibody (Mab) against respiratory syncytial virus (RSV). The humanised
 CC antibody is useful for preventing or treating a respiratory syncytial
 CC virus infection. The antibody is also useful for diagnosing RSV
 CC infection. The antibody can be injected which is preferable to prior art
 CC treatment methods involving intravenous transfusions. The present
 CC sequence represents a human-murine chimeric antibody.
 XX SQ Sequence 129 AA;
 CC Query Match 90.9%; Score 510; DB 5; Length 129;
 CC Best Local Similarity 88.8%; Pred. No. 6e-32; Mismatches 8; Indels 0; Gaps 0;
 CC Matches 95; Conservative 8; Mismatches 4;
 CC AC
 QY 1 DIQMTQSPSSLASAVGDRVITICKASQDINISLYSLWQOKQAKPILIVRANLVDGVPS 60
 CC Db 23 DIQMTQSPSTLUSASVGDRTTICKASQDINISLYSLWQOKQAKPILIVRANLVDGVPS 82
 CC QY 61 RRSGGSSGQDYVLTISLSQLPDDPATVYCLQDDEFPYTFGGTKVIEK 107
 CC Db 83 RPSSGSGSGTERTLTISLSQLPDDPATVYCLQDDEFPYTFGGTKVIEK 129
 RESULT 12
 AAW58478
 ID AAW58478 standard; protein; 107 AA.
 XX AC
 AC AAW58478;
 XX DT 18-AUG-1998 (first entry)
 XX DE Humanised anti-CD5 immunoglobulin H65 light chain variable region #1.
 XX KW Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
 KW depletion; cytotoxic; immunoenzyme; fusion protein; porin;
 KW autoimmune disease; rheumatoid arthritis; type I diabetes.
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX US5770196-A.
 XX PD 23-JUN-1998.
 XX PD 07-JUN-1995; 95US-00472788.
 XX PF 13-DEC-1991; 91US-00808464.
 XX PR 14-DEC-1992; 92US-0010906.
 XX BR 23-JUN-1993; 93US-00082842.
 XX PA (XOMA) XOMA CORP.
 XX PR Studnicka GM;
 XX DR
 XX WPI; 1998-376744/32.
 XX Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies with
 PT humanised variable regions.
 XX Claim 1; Col 63-64; 77pp; English.
 XX A method has been developed of depleting CD5+ cells in an animal. The
 CC method comprises administering a cytotoxic protein containing a modified
 CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig

CC molecule or an immunoconjugate or fusion protein containing an anti-CD5 Ig molecule, and where the modified Ig variable domain comprises at least one of (a) a modified light chain variable region (see AAW8478 or AAW8480), and (b) a modified heavy chain variable region (see AAW58479 or AAW58481), where AAW8478 and AAW58479 are humanised forms of the H65 light and heavy chain variable domains with low risk amino acid substitutions [i.e. low risk of reducing antigen-binding specificity.] and AAW8480 and AAW58481 are humanised forms of the H65 light and heavy chain variable domains with moderate risk amino acid substitutions and are present in humanised H65 antibody h65 (NCC HB 11206). The method is useful for treating autoimmune diseases, especially systemic lupus erythematosus, rheumatoid arthritis, psoriasis or type I diabetes. The present sequence represents a specifically claimed humanised anti-CD5 immunoglobulin H65 light chain variable region

XX SQ Sequence 107 AA;

Query Match 89.5%; Score 502; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 2.1e-31; Mismatches 6; Indels 0; Gaps 0;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQWQSPPSLSASVGDRVITICKAQDINSYLSWFQOKPGKSPTRLIVRNLVGVPS 60
Db 1 DIQWQSPPSMSASIGDRVITICKAQDINSYLSWFQOKPGKSPTRLIVRNLVGVPS 60

QY 61 RFSGSGSGDQYDTISLOQEDFATYCQYDQYDESPWTFGGKLEIK 107
Db 61 RFSGSGSGDQYDTISLOQEDFATYCQYDQYDESPWTFGGKLEIK 107

RESULT 13
AD101168
ID AD101168 standard; protein; 107 AA.
XX AC AD101168:
XX DT 22-APR-2004 (first entry)
XX Murine monoclonal antibody H65 humanised light chain VL protein 1.
KW variable domain; immunosuppressive; dermatological; antiinflammatory;
KW antidiabetic; antithyroid; antisporadic; antirheumatic; antiarthritic;
KW neuroprotective; antiulcer; antianæmic; fungicide; virucide; autoimmune;
KW systemic lupus erythematosus; lupus nephritis; Scleroderma; morphea;
KW lichen planus; rheumatoid arthritis; spondylarthritis; thyroiditis;
KW pemphigus vulgaris; diabetes mellitus type 1; progressive systemic sclerosis; aplastic anaemia; myasthenia gravis;
KW myositis; polymyositis; dermatomyositis; Sjögren's disease; collagen vascular disease, polyarthritis, inflammatory bowel disease including Crohn's disease and ulcerative colitis; multiple sclerosis; psoriasis and primary biliary cirrhosis. Furthermore, the polypeptide may be utilised to address other diseases mediated by T cells, such as tissue transplant rejection and graft versus host disease, as well as diseases caused by viral or fungal infection. The current sequence is that of the murine antibody variable domain protein of the invention.

XX SQ Sequence 107 AA;

Query Match 89.5%; Score 502; DB 8; Length 107;
Best Local Similarity 88.8%; Pred. No. 2.1e-31; Mismatches 6; Indels 0; Gaps 0;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQWQSPPSLSASVGDRVITICKAQDINSYLSWFQOKPGKSPTRLIVRNLVGVPS 60
Db 1 DIQWQSPPSMSASIGDRVITICKAQDINSYLSWFQOKPGKSPTRLIVRNLVGVPS 60

QY 61 RFSGSGSGDQYDTISLOQEDFATYCQYDQYDESPWTFGGKLEIK 107
Db 61 RFSGSGSGDQYDTISLOQEDFATYCQYDQYDESPWTFGGKLEIK 107

RESULT 14
AY52724
ID AY52724 standard; protein; 107 AA.
XX AC AY52724:
XX DT 26-JAN-2000 (first entry)
XX DE Humanised ATR-5 L chain V region version "b1" protein sequence.
XX KW Human tissue factor; TP; humanised; antibody; mouse monoclonal antibody; ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC; disseminated intravascular coagulation; immunogenicity; chimeric.
XX OS Synthetic.
OS Homo sapiens.
XX PN WO951743-A1.
XX PD 14-OCT-1999.
XX PP 02-APR-1999; 99WO-JP001768.
XX PR 03-APR-1998; 98JP-00091850.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PI Studnicka GM;
XX DR WPI; 2004-04-2226/04.

PT Sato K, Adachi H, Yabuta N;
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 DR XX
 DR PI
 XX N-PSDB; AA233089.
 PT XX
 PT Humanised antibody recognizing human tissue factor, used for treatment of
 disseminated intravascular coagulation.
 XX PS Claim 18, Page 259, 291pp; Japanese.
 CC The present invention describes chimeric antibody (Ab) heavy (H) chains
 containing the variable region of the H chain of a mouse monoclonal Ab
 recognising human tissue factor (hTF) and the constant region of the H
 chain of a human Ab. The variable region is one of six specified
 sequences (which are the H chain variable regions from mouse monoclonal
 Ab's ATR-2, 3, 4, 5, 7 or 8). Also described are chimeric Ab light (L) chains
 containing the variable region of the L chain of a mouse monoclonal Ab
 recognising human tissue factor (hTF) and the constant region of the L
 chain of a human Ab, the variable region being one of six specified
 sequences (which are the L chain variable regions from mouse monoclonal
 Ab's ATR-2, 3, 4, 5, 7 or 8). The chimeric Ab's can be used for the treatment
 and prevention of thrombotic disease, especially of disseminated
 intravascular coagulation (DIC). The humanised antibody has the high hTF
 immunogenicity. A2Z33001 to A2Z33091 and Y527007 to A4Y52767 represent
 sequences used in the exemplification of the present invention
 XX SQ Sequence 107 AA;

Query Match Best Local Similarity 89.9%; Score 499; DB 2; Length 107;
 Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSVLSWFOQKQKAPKTLIYRANLVDGVPs 60
 Db 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSVLSWFOQKQKAPKTLIYRANLVDGVPs 60
 Qy 61 RFSGSGSGQDYLTISLQPEDFATYCLQDDEPYTGGKTVKEIK 107
 Db 61 RFSGSGSGQDYLTISLQPEDFATYCLQDDEPYTGGKTVKEIK 107

RESULT 15

A2B74985
 ID A2B74985 standard; protein; 107 AA.
 XX AC A2B74985;
 XX DT 16-JUL-2001 (first entry)
 DE Humanised ATR-5 L chain V region version b1 SEQ ID NO:96.
 KW Mouse; human; humanised; monoclonal antibody; tissue factor; TF;
 prevention; blood coagulation; tumour; ATR-5; anticoagulant;
 thrombolytic; infection; venous thrombosis; arterial thrombosis;
 vascular medial thickening; accelerated blood coagulation; thrombosis;
 blood vessel thickening.
 XX OS Mus sp.
 OS Homo sapiens.
 XX PN WO200124626-A1.
 XX PD 12-APR-2001.
 XX PP 29-SEP-2000; 2000WO-JP006802.

XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX DR XX
 DR PI
 XX N-PSDB; AA233089.
 PT XX
 PT Mouse model for sustained accelerated blood coagulation, thrombosis and blood vessel thickening.
 XX PS Example; Page 165-187, 202pp; Japanese.
 CC The present invention describes an experimental animal model transplanted
 with animal cells expressing human tissue factor or a fragment of it,
 with accelerated blood coagulation. Also described are: (1) selecting an
 animal model; (2) screening for anti-thrombotics; (3) treatment and
 prevention of accelerated blood coagulation; and (4) polyclonal and
 monoclonal antibodies or their fragments. The animal model is useful in
 the search and development of remedies for diseases associated with the
 sustained acceleration of blood coagulation such as that caused by
 infection, venous thrombosis, arterial thrombosis and disease caused by
 vascular medial thickening. Antibodies from the present invention against
 human tissue factor (TF) (e.g. anti mouse monoclonal antibody ATR-5 and
 humanised ATR-5) can be used in the treatment and prevention of
 accelerated blood coagulation, thrombosis and blood vessel thickening.
 CC ABP87917 to AAB74985 and AAB74990 represent nucleotide and
 protein sequences which are used in the exemplification of the present
 invention
 XX SQ Sequence 107 AA;

Query Match Best Local Similarity 89.9%; Score 499; DB 4; Length 107;
 Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSVLSWFOQKQKAPKTLIYRANLVDGVPs 60
 Db 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSVLSWFOQKQKAPKTLIYRANLVDGVPs 60
 Qy 61 RFSGSGSGQDYLTISLQPEDFATYCLQDDEPYTGGKTVKEIK 107
 Db 61 RFSGSGSGQDYLTISLQPEDFATYCLQDDEPYTGGKTVKEIK 107

Search completed: December 29, 2004, 17:57:35
 Job time : 74.5428 Secs

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:38:43 ; Search time 73.8584 Seconds
 (without alignments)

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CLQYDEFPYTFGGTIKEVK 107

Scoring table: Blosum62

Searched: Gapop 10.0 , Gapext 0.5

1825181 seqs., 57374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0‡

Maximum Match 100‡

Listing first 45 summaries

* UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	494	88.1	214 2 O9R1A5	O9R1A5 mus musculus
2	494	88.1	235 2 O7TS98	O7TS98 mus musculus
3	474	84.5	128 1 KVI5_MOUSE	KVI5_MOUSE
4	449	80.0	108 1 KV1Y_HUMAN	KV1Y_HUMAN
5	446	79.5	235 2 Q7Z3V4	Q7Z3V4 homo sapien
6	445	79.3	236 2 Q6GMK8	Q6GMK8 homo sapien
7	444	79.1	108 1 KV1B_HUMAN	KV1B_HUMAN
8	444	79.1	235 2 Q7TMK3	Q7TMK3 mus musculus
9	443	79.0	108 1 KV1V_HUMAN	KV1V_HUMAN
10	442	78.8	108 1 KV1P_HUMAN	KV1P_HUMAN
11	442	78.8	115 1 KV5P_MOUSE	KV5P_MOUSE
12	441	78.6	108 1 KVIR_HUMAN	KVIR_HUMAN
13	439	78.3	1 KV1O_HUMAN	KV1O_HUMAN
14	437	77.9	235 2 O6GMK9	O6GMK9 homo sapien
15	436.5	77.8	107 2 Q96SA9	Q96SA9 homo sapien
16	435	77.5	108 2 Q9UL70	Q9UL70 homo sapien
17	435	77.5	235 2 O6PIH7	O6PIH7 homo sapien
18	435	77.5	236 2 O6GMW1	O6GMW1 homo sapien
19	435	77.5	236 2 AAH3141	AAH3141 homo sapien
20	433	77.2	108 2 Q9UL77	Q9UL77 homo sapien
21	432	77.0	108 1 KV1H_HUMAN	KV1H_HUMAN
22	432	77.0	236 2 O6GMX0	O6GMX0 homo sapien
23	427.5	76.2	107 1 KV1D_HUMAN	KV1D_HUMAN
24	427	76.1	108 1 KV1A_HUMAN	KV1A_HUMAN
25	427	76.1	108 1 KV1G_HUMAN	KV1G_HUMAN
26	427	76.1	108 1 KV1M_HUMAN	KV1M_HUMAN
27	426	75.9	108 1 KV1L_HUMAN	KV1L_HUMAN
28	423	75.4	108 1 KV1E_HUMAN	KV1E_HUMAN
29	420	74.9	108 1 KV1F_HUMAN	KV1F_HUMAN
30	74.9	108 1 KV1Q_HUMAN	KV1Q_HUMAN	
31	74.7	108 1 KV1I_HUMAN	KV1I_HUMAN	

RESULT 1

SEQUENCE FROM N.A.	RA	Wilde K.G., Yu X., Ekmamoddoullah A.K.M., Misra S.;
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF152371; ADU40242.1; -.	
DR	PIR; PH1065; PH1065.	
DR	PDB; 1AHW; X-ray; D=.	
DR	PDB; 1CIC; X-ray; A/C=1-214.	
DR	PDB; 1K6Q; X-ray; L=1-210.	
DR	GO; GO:0005634; C:nucleus; IEA.	
DR	GO; GO:0003700; P:transcription factor activity; IEA.	
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.	
DR	InterPro; IPR001356; Homeobox.	
DR	InterPro; IPR01110; Ig-like.	
DR	InterPro; IPR0597; Ig-cl.	
DR	InterPro; IPR03006; Ig MHC.	
DR	InterPro; IPR03596; Ig V.	
DR	Pfam; PF07554; Cl-set; 1.	
DR	Pfam; PF00047; Ig; 1.	
DR	PRINTS; PR00024; HOMEBOX.	
DR	SMART; SH00405; IgV; 1.	
DR	PROSITE; PS50356; Ig_LIKE; 2.	
DR	PROSITE; PS50290; Ig_MHC; UNKNOWN_1.	
FT	NON_TER	1
FT	NON_TER	1
FT	NON_TER	214
FT	NON_TER	214
FT	NON_TER	214 AA; 23922 MW; 52BA205FDE995B2A CRC64;
SEQNCE	214 AA;	214

Best Local Similarity 86.0%; **Score** 494; **DB** 2; **Length** 214; **Matches** 92; **Conservative** 9; **Mismatches** 6; **Indels** 0; **Gaps** 0

Qry 1 DIQMTQSPSSLSASVGRVTITKASODINSYLSWFOOKRGKAPETLYRANLVDGVP5 60

Db 1 DIQMTQSPSSLSASVGRVTITKASODINSYLSWFOOKRGKAPETLYRANLVDGVP5 60

Qry 61 RFSAGSGGQDYITISLQPRTATYCYQDPERPYFEGGTQKRIK 107

Db 61 RFSAGSGGQDYITISLQPRTATYCYQDPERPYFEGGTQKRIK 107

RESULT 2

Q7NS98	PRELIMINARY;	PRT;	236 AA.
ID			
AC			
DT	01-OCT-2003 (TREMbrel; 25, Created)		
DT	01-OCT-2003 (TREMbrel; 25, Last sequence update)		
DT	01-MAR-2004 (TREMbrel; 26, Last annotation update)		
DB	Anti-colorectal carcinoma light chain.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC	NCBI_TaxID=1090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE:9333497; PubMed:8372513;		
RA	Tonge D.W., Henman J.F., Greene A.R., Lee I.D., Edge M.D.;		
RT	"Cloning and characterization of 116NS19.9 heavy and light chain cDNAs and expression of antibody fragments in Escherichia coli.",		
RL	Year Immunol. 7:56-62(1993).		
DR	PIBMU; S65921; AAB28160_1; -.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR03591; Ig_v.		
DR	InterPro; IPR003006; Ig_MIC.		
DR	Pfam; PF07554; C1-set; T.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IgV; 1.		
DR	PROSITE; PS50835; Ig_LIKE; 2.		
DR	PROSITE; PS00290; Ig_MHC; UNKNOWN 1.		
SQ	SEQUENCE 236 AA; 26454 MW; 2C86EBP5EA1OP4C CRC64;		
Query Match	88.1%; Score 494; DB 2; Length 236;		
Best Local Similarity	86.9%; Pred. No. 3. 9e-43;		
Matches	93; Conservative 8; Mismatches 6; Indels 0; Gaps 0;		
QY	1 DIQMTQSPSISASVSDRVITCKQSODINSYLSWFOQKRGKAKPTLYRANLVGDYPS 60		
Db	23 DIKMTQSPSSMVASLGERTVITCKQSODINSYLSWFOQKRGKSPKTLYRANLVGDYPS 82		
QY	61 RFSGSSGQDQTTSLOPDEFTATYCQCYDEFPYTRGGTKWEIK 107		
Db	83 RFSGSSGQDQTTSLOPDEFTATYCQCYDEFPYTRGGTKWEIK 129		
RESULT 3			
KV5E_MOUSE	STANDARD;	PRT;	128 AA.
ID			
AC	P01637;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	15-JUL-1986 (Rel. 01, Last sequence update)		
DR	Ig kappa chain V-V region TI precursor.		
OS	Mus musculus (Mouse).		
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromyath; Muridae; Mus.		
OC	NCBI_TaxID=1090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE:8105342; PubMed:6776411;		
RA	Attenburger W., Steinmetz M., Zachau H.G.;		
RT	"Functional and non-functional Joining in immunoglobulin light chain genes of a mouse myeloma.",		
RT	Nature 287:603-607(1980).		
RL	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	EMBL; V00772; CA24150_1; -.		
DR	PIR; A01920; KV5T1.		
DR	HSSP; P80362; IWTL;	DR	
DR	InterPro; IPR007110; Ig-like.	DR	
DR	InterPro; IPR03596; Ig_v.	DR	
DR	Pfam; PF00047; Ig_v; 1.	DR	
DR	SMART; SM0046; Ig_v; 1.	DR	
DR	PROSITE; PS50835; Ig_LIKE; 1.	DR	
DR	Immunglobulin V region; Signal.	FT	
FT	SIGNAL 1	20	
FT	CHAIN 21	128	Ig kappa chain V-V region T1.
FT	DOMAIN 21	43	
FT	DOMAIN 44	54	Complementarity-determining-1.
FT	DOMAIN 55	69	Framework-2.
FT	DOMAIN 70	76	Complementarity-determining-2.
FT	DOMAIN 77	108	Framework-3.
FT	DOMAIN 109	117	Complementarity-determining-3.
FT	DOMAIN 118	127	Framework-4.
FT	DISULFID 43	108	By similarity.
FT	NON_TER 128	128	
SQ	SEQUENCE 128 AA; 14385 MW; AFAS563D31BB7E05 CRC64;		
Query Match	84.5%; Score 474; DB 1; Length 128;		
Best Local Similarity	81.3%; Pred. No. 2.3e-41;		
Matches	87; Conservative 13; Mismatches 0; Indels 0; Gaps 0;		
QY	1 DIQMTQSPSISASVSDRVITCKQSODINSYLSWFOQKRGKAKPTLYRANLVGDYPS 60		
Db	21 DIKMTQSPSSMVASLGERTVITCKQSODINSYLSWFOQKRGKSPKTLYRANLVGDYPS 80		
QY	61 RSSGSSGQDQTTSLOPDEFTATYCQCYDEFPYTRGGTKWEIK 107		
Db	81 RFSGSSGQDQTTSLOPDEFTATYCQCYDEFPYTRGGTKWEIK 127		
RESULT 4			
KVLY_HUMAN	STANDARD;	PRT;	108 AA.
ID	KVLY_HUMAN		
AC	P80362;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	01-OCT-2004 (Rel. 45, Last annotation update)		
DR	Ig kappa chain V-I region WAT.		
OS	Homo sapiens (Human).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).		
RX	MEDLINE:25086080; PubMed:793911;		
RA	Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Bultz M., Solomon A., Stevens F.J., Schiffer M.,		
RT	Comparison of crystal structures of two homologous Proteins: structural origin of altered domain interactions in immunoglobulin light-chain dimers.",		
RT	Biochemistry 33:14848-14857(1994).		
RL	Biocchemistry 33:14848-14857(1994).		
RN	[2]		
RP	SEQUENCE OF 1-35.		
RX	MEDLINE:81267384; PubMed:6167731;		
RA	Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,		
RA	Popp R.A., Solomon A.;		
RT	"Characterization and preliminary crystallographic data on the VL-related fragment of the human κI Bence Jones protein Wat.",		
RT	J. Mol. Biol. 147:185-193(1981).		
CC	-- MISCELLANEOUS: This is a Bence-Jones protein.		
DR	PDB; IWTL; X-ray; A/B1-L08.		
DR	GO; GO:0005576; C: extracellular; NAS.		
DR	GO; GO:0003623; P: antigen binding; NAS.		
DR	GO; GO:006555; P: immune response; NAS.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR03591; Ig_v.		
DR	Pfam; PF00047; Ig_v; 1.		
DR	SMART; SM0046; Ig_v; 1.		
DR	PROSITE; PS50835; Ig_LIKE; 1.		
DR	3D-structure; Bence-Jones protein; Direct protein sequencing;		

KW Immunoglobulin V region.
PT DOMAIN 1 23 Framework-1.
PT DOMAIN 24 34 Complementarity-determining-1.
PT DOMAIN 35 49 Framework-2.
PT DOMAIN 50 56 Complementarity-determining-2.
PT DOMAIN 57 88 Framework-3.
PT DOMAIN 89 97 Complementarity-determining-3.
PT DOMAIN 98 107 Framework-4.
PT DISLFID 23 88 By similarity.
PT CONFLICT 30 31 TN -> SD (in Ref. 2).
PT STRAND 4 7
PT STRAND 10 13
PT TURN 15 16
PT STRAND 19 25
PT TURN 30 31
PT STRAND 33 38
PT TURN 40 41
PT STRAND 45 49
PT TURN 50 52
PT STRAND 53 54
PT TURN 56 57
PT TURN 60 61
PT STRAND 62 67
PT TURN 68 69
PT STRAND 70 75
PT HELIX 80 82
PT STRAND 84 90
PT STRAND 98 98
PT STRAND 102 106
PT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAB697 CRC64;
Db Query Match 80.0%; Score 449; DB 1; Length 108; Best Local Similarity 79.4%; Pred. No. 7.7e-39; Mismatches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
Qy 61 RFSGSGSGGDTTSSLOPEDFATYCYCQYDDEPFYTFGGTKVBIK 107
Db 61 RFSGSGSGGDTTSSLOPEDFATYCYCQYDDEPFYTFGGTKVBIK 107
RESULT 5
ID 0723Y4 PRELIMINARY; PRT; 236 AA.
AC Q723Y4; 25. Created)
DT 01-OCT-2003 (Tremblel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID: 9606;
[1]
SEQUENCE FROM N.A.
PT TISSUE=Skeletal Muscle;
PT MEDLINE:22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Shuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Blat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalobos D.K., Muñoz D.M., Sodegren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madden A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marras M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.; Submitted (Mar-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC005312; AAH05332.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003557; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003595; Ig_V.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PR00047; Ig; 1.
DR SMART; SM0006; Ig_V.
DR PROSITE; PS50835; Ig_LIKE; 2.
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
KW Hypothetical protein.
PT SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
Db Query Match 79.5%; Score 446; DB 2; Length 236; Best Local Similarity 79.4%; Pred. No. 3.9e-36; Mismatches 12; Indels 0; Gaps 0;
Db 23 DIQMTQSPSSLSASVGDRVITCKASQDINSYLSWFOQRQQPKVPLIVGASSLQSIVS 82
Qy 61 RFSGSGSGGDTTSSLOPEDFATYCYCQYDDEPFYTFGGTKVBIK 107
Db 61 RFSGSGSGGDTTSSLOPEDFATYCYCQYDDEPFYTFGGTKVBIK 107
RESULT 6
ID 06GMX8 PRELIMINARY; PRT; 236 AA.
AC Q6GMX8; 27. Created)
DT 05-JUL-2004 (Tremblel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID: 9606;
[1]
RP TISSUE=Primary B-Cells;
RA MEDLINE:22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Shuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Blat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalobos D.K., Muñoz D.M., Sodegren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madden A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smilus D.E., Scherich A., Schein J.E.,
RA Jones S.J.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[2]

SEQUENCE FROM N.A.

TISSUE=Primary B-Cells;

R.A. Straubberg R.,

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; BC073764; AAH73764.1; -.

DR InterPro; IPR003599; Ig-like.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig_v.

DR SMART; SM00406; Ig_MHC.

DR PROSITE; PS00835; Ig_LIKE.

KW Immuno-globulin V region.

FT 3D-structure; Bence-Jones protein; Direct protein sequencing;

FT DOMAIN 24 34 23 Framework-1.

FT DOMAIN 35 49 Complementarity-determining-1.

FT DOMAIN 50 56 Framework-2.

FT DOMAIN 57 88 Complementarity-determining-2.

FT DOMAIN 89 97 Framework-3.

FT DOMAIN 98 107 Complementarity-determining-3.

FT DISULFID 23 88 Framework-4.

FT STRAND 4 5 By similarity.

FT STRAND 10 13

FT TURN 15 16

FT STRAND 19 25

FT TURN 30 31

FT STRAND 33 38

FT TURN 40 41

FT STRAND 44 49

FT TURN 50 52

FT STRAND 53 54

FT TURN 56 57

FT STRAND 60 61

FT TURN 62 67

FT STRAND 68 69

FT TURN 70 75

FT HELIX 80 82

FT STRAND 85 90

FT STRAND 97 98

FT STRAND 102 105

FT NON TER 108 108

SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6R6FB9 CRC64;

Query Match 79.1%; Score 444; DB 1; Length 108;

Best Local Similarity 79.4%; Pred. No. 2; Mismatches 0;

Matches 85; Conservative 7; MisMatches 15; Indels 0; Gaps 0;

DR 1 DIOMTOSPPSSASAVQDRVTICKASQDINSYLSWFQORPGKAPTKLYRANLVDPGVS 60

Db 23 DIOMTOSPPSSASAVQDRVTICKASQDINSYLSWFQORPGKAPTKLYRANLVDPGVS 82

Qy 61 RFSGGGSGQQYLTISLIQPEDFATYYCQYDLYRPTYEGGGRVKEIK 107

Db 83 RFSGGGSGQQYLTISLIQPEDFATYYCQYDLYRPTYEGGGRVKEIK 129

RESULT 7

KV1B HUMAN

ID KV1B_HUMAN STANDARD; PRT; 108 AA.

AC P01594; Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DB 1g kappa chain V-T region AU.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OK NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=72189444; PubMed=5028201;

RA Schiechl H., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal protein Au";

RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";

RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).

RN [2]

X-RAY CRYSTALLOGRAPHY.

RX MEDLINE=77022433; PubMed=1234024;

RA Fehlhammer H., Schiffrer M., Bopp O., Colman P.M., Lattman E.B., Schwager P., Steigemann W., Schramm H.J.;

RT "The structure determination of the variable portion of the Bence-Jones protein Au";

RL Biophys. Struct. Mech. 1:139-146(1975).

-I MISCELLANEOUS: The structure of the V region was determined by molecular replacement methods using the known structure of the V region of the kappa chain REL.

CC -I MISCELLANEOUS: This is a Bence-Jones protein.

CC PIR_A91653; KIHNU.

PDB_1U55 X-ray; A=1-107.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR00596; Ig_v.

DR SMART; SM00406; Ig_MHC.

DR PROSITE; PS00835; Ig_LIKE.

KW Immuno-globulin V region.

FT 3D-structure; Bence-Jones protein; Direct protein sequencing;

FT DOMAIN 24 34 23 Framework-1.

FT DOMAIN 35 49 Complementarity-determining-1.

FT DOMAIN 50 56 Framework-2.

FT DOMAIN 57 88 Complementarity-determining-2.

FT DOMAIN 89 97 Framework-3.

FT DOMAIN 98 107 Complementarity-determining-3.

FT DISULFID 23 88 Framework-4.

FT STRAND 4 5 By similarity.

FT STRAND 10 13

FT TURN 15 16

FT STRAND 19 25

FT TURN 30 31

FT STRAND 33 38

FT TURN 40 41

FT STRAND 44 49

FT TURN 50 52

FT STRAND 53 54

FT TURN 56 57

FT STRAND 60 61

FT TURN 62 67

FT STRAND 68 69

FT TURN 70 75

FT HELIX 80 82

FT STRAND 85 90

FT STRAND 97 98

FT STRAND 102 105

FT NON TER 108 108

SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6R6FB9 CRC64;

Query Match 79.1%; Score 444; DB 1; Length 108;

Best Local Similarity 79.4%; Pred. No. 2; Mismatches 0;

Matches 85; Conservative 7; MisMatches 15; Indels 0; Gaps 0;

DR 1 DIOMTOSPPSSASAVQDRVTICKASQDINSYLSWFQORPGKAPTKLYRANLVDPGVS 60

Db 1 DIOMTOSPPSSASAVQDRVTICKASQDINSYLSWFQORPGKAPTKLYRANLVDPGVS 82

Qy 61 RFSGGGSGQQYLTISLIQPEDFATYYCQYDLYRPTYEGGGRVKEIK 107

Db 61 RFSGGGSGQQYLTISLIQPEDFATYYCQYDLYRPTYEGGGRVKEIK 129

RESULT 8

OPTM3

OPTM3 PRELIMINARY; PRT; 236 AA.

R.P. OPTM3; Q7TM3; PRELIMINARY; PRT; 236 AA.

RP 01-OCT-2003 (Tremblrel. 25, Created)

DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)

DB 01-MAR-2004 (Tremblrel. 26, Last annotation update)

OS Hypothetical protein.

OS Mus musculus (Mouse).

OC Balaustia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CZECH II;

RC TISSUE=Mammal tumor metastatized to lung. Tumor arose spontaneously;

RC MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Degege J.G., Schueler G.D., Altschuler S.F., Zeberg B., Buetow K.H., Schaefer C.F., Blatt N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA	Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E., Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Locullano N.A., Peters G.J., Abramson R.D., Mulahay S.J., Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunnarino P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.M., Sodergren B.J., Lu X., Gibbs R.A., Gibbs R.J., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G., Blatley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzwiniski M.I., Skalska U., Smalius D.E., Schnurch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL	RT
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CZCZ II;
RC	TISSUE=Summary tumor metastatized to lung. Tumor arose spontaneously;
RA	Strausberg R.; Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BCCS5906; AAH55905.1; -.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig_c1.
DR	InterPro; IPR003065; Ig_MHC.
DR	InterPro; IPR03595; Ig_v.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SM00406; IgV; 1.
DR	PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
KW	Hypothetical protein.
SQ	SEQUENCE 236 AA; MW: 0DB3488AAA6396P CRC64;
Query Match	79.1%; Score 444; DB 2; Length 108;
Best Local Similarity	78.5%; Pred. No. 6.3e-38;
Matches	84; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
Qy	1 DIQWTOQSPSSLASVGDRVTICKASQDINSYLSWFQQPKGKAPRTLYRANRVLGVPS 60
Db	23 DIKWTQSPSSLYASLGERVITCKASODIKSYLSWQKEWKSPKTLIYTSLADGVPS 82
Qy	61 RFSSSGSGDQYLTISLQPEDFATYCYQOYDFFPYTGGGTKVBIK 107
Db	61 RFTGSGSGDFILTISLQPEDFATYCYQOYNSIPYFGQGTKVBIK 107
RESULT 9	KV1P_HUMAN
ID	KV1P_HUMAN
AC	AC01608;
DT	DT 21-JUL-1986 (Rel. 01, Created)
DT	DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT	DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB	DB Ig kappa chain V-I region Roy.
OS	OS Homo sapiens (Human)
OC	OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	OX NCBI_TaxID=9606;
RN	RN [1]
RP	SEQUENCE.
RX	RX MEDLINE-68362076; PubMed=5595110;
RA	RA Hildebrandt N.;
RA	RA Steinmann N.;
RA	RA "Chemical structure of 2 kappa-Type Bence Jones proteins (Roy and Cum.)", Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN	RN [2]
RP	RP REVISIONS TO 39 AND 41.
RA	RA Hildebrandt N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Watanabe S.;
RL	RL (In) Franek F., Shugar D. (eds.); Gamma Globulins: structure and function, pp.57-74, Academic Press, New York (1969).
RL	RL -1- MISCELLANEOUS: The C region of this chain has the INV (1,2) marker.
CC	CC Homo sapiens (Human)
OS	OS Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	OC Homo sapiens (Human)
NCBI_TaxID=9606;	RN
RP	SEQUENCE.
RX	RX MEDLINE-6174817; PubMed=3003240;
RA	RA Dwulet F.E., O'Conor T.P., Benson M.D.; "amyloid protein (BAN)";
RT	RT "Polymorphism in a kappa I primary (Al) amyloid protein (BAN)." Mol. Immunol. 23:73-78(1986).
RL	RL PIR; A01878; KIHURN.
DR	DR HSSP; P80362; IWTL.
DR	DR GO; GO:0005576; C:extracellular; NAS.
DR	DR GO; GO:0003823; F:immune binding; NAS.
DR	DR GO; GO:0006955; P:immune response; NAS.
DR	DR InterPro; IPR007110; Ig-like.
DR	DR InterPro; IPR003596; Ig_v.
DR	DR Pfam; PF00047; Ig_1.
DR	DR SMART; SM00406; IgV; 1.
DR	DR PROSITE; PS00293; F:antigen binding; NAS.
DR	DR GO; GO:0006555; F:immune response; NAS.
DR	DR InterPro; IPR007110; Ig-like.
DR	DR HSSP; P01607; IBW.
DR	DR GO; GO:0005576; C:extracellular; NAS.
DR	DR GO; GO:0003823; F:immune binding; NAS.
DR	DR SMART; SM00406; IgV; 1.
DR	DR PROSITE; PS00293; F:antigen binding; NAS.
KW	Bence-Jones protein; Direct protein sequencing.
KW	Immunglobulin V region.
FT	FT DOMAIN 1 23 Framework-1.
FT	FT DOMAIN 24 34 Complementarity-determining-1.
FT	FT DOMAIN 50 56 Framework-2.
FT	FT DOMAIN 57 88 Complementarity-determining-2.
FT	FT DOMAIN 89 97 Framework-3.
FT	FT DOMAIN 98 107 Complementarity-determining-3.
FT	FT DOMAIN 107 88 Framework-4.
FT	FT DISNUFD 23 88 By similarity.
FT	FT NON_TER 108 108 MW: CD3FD944FE96FD37 CRC64;
SQ	SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;
Query Match	79.0%; Score 443; DB 1; Length 108;
Best Local Similarity	76.6%; Pred. No. 3.2e-38;
Matches	82; Conservative 13; Mismatches 12; Indels 0; Gaps 0;
Qy	1 DIQWTOQSPSSLASVGDRVTICKASQDINSYLSWFQQPKGKAPRTLYRANRVLGVPS 60
Db	1 DIQWTOQSPSSLASVGDRVTICKASQDINSYLSWFQQPKGKAPRTLYRANRVLGVPS 60
Qy	61 RFSSSGSGDQYLTISLQPEDFATYCYQOYDFFPYTGGGTKVBIK 107
Db	61 RFTGSGSGDFILTISLQPEDFATYCYQOYNSIPYFGQGTKVBIK 107
RESULT 10	KV1P_HUMAN
ID	KV1P_HUMAN
AC	AC P01608;
DT	DT 21-JUL-1986 (Rel. 01, Created)
DT	DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT	DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB	DB Ig kappa chain V-I region Roy.
OS	OS Homo sapiens (Human)
OC	OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	OX NCBI_TaxID=9606;
RN	RN [1]
RP	SEQUENCE.
RX	RX MEDLINE-68362076; PubMed=5595110;
RA	RA Hildebrandt N.;
RA	RA Steinmann N.;
RA	RA "Chemical structure of 2 kappa-Type Bence Jones proteins (Roy and Cum.)", Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN	RN [2]
RP	RP REVISIONS TO 39 AND 41.
RA	RA Hildebrandt N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Watanabe S.;
RL	RL (In) Franek F., Shugar D. (eds.); Gamma Globulins: structure and function, pp.57-74, Academic Press, New York (1969).
RL	RL -1- MISCELLANEOUS: The C region of this chain has the INV (1,2) marker.
CC	CC Homo sapiens (Human)
OS	OS Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	OC Homo sapiens (Human)
NCBI_TaxID=9606;	RN
RP	SEQUENCE.
RX	RX MEDLINE-6174817; PubMed=3003240;
RA	RA Dwulet F.E., O'Conor T.P., Benson M.D.; "amyloid protein (BAN)";
RT	RT "Polymorphism in a kappa I primary (Al) amyloid protein (BAN)." Mol. Immunol. 23:73-78(1986).
RL	RL PIR; A01878; KIHURN.
DR	DR HSSP; P80362; IWTL.
DR	DR GO; GO:0005576; C:extracellular; NAS.
DR	DR GO; GO:0003823; F:immune binding; NAS.
DR	DR GO; GO:0006955; P:immune response; NAS.
DR	DR InterPro; IPR007110; Ig-like.
DR	DR InterPro; IPR003596; Ig_v.
DR	DR Pfam; PF00047; Ig_1.
FT	FT DOMAIN 1 23 Framework-1.
FT	FT DOMAIN 24 34 Complementarity-determining-1.
FT	FT DOMAIN 50 56 Framework-2.
FT	FT DOMAIN 57 88 Complementarity-determining-3.
FT	FT DOMAIN 89 97 Framework-4.

PT DOMAIN 89 97 Complementarity-determining-3.
 PT DOMAIN 98 107 Framework-4.
 PT DISULFD 23 88 By similarity.
 PT NON TER 108 108
 SQ SEQUENCE 108 AA; 11782 MW; FSACED5A313DF3A CRC64;
 Query Match 78.8%; Score 442; DB 1; Length 108;
 Best Local Similarity 77.6%; Pred. No. 4,1e-38;
 Matches 83; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
 QY 1 DIQWQSPSSLSASVGDRVTITCKASODINSLSWFOQPKAKPILYRANRLVGVPS 60
 Db 1 DIQWQSPSSLSASVGDRVTITCKASODINSLSWFOQPKAKPILYRANRLVGVPS 80
 QY 61 RFSGSGSGDVTISQPERPATYCLQDEFP 95
 Db 81 RFSGSGSGDVTISQPERPATYCLQDEFP 115
 RESULT 11
 KV5_MOUSE STANDARD; PRT; 115 AA.
 ID KV5_MOUSE STANDARD; PRT; 108 AA.
 AC P01638;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DB DB IG kappa chain V-I region WEA.
 OS OS Homo sapiens (Human).
 OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 OC OC NCBI_TAXID=9606;
 RN RN [1]
 RP RP SEQUENCE.
 RX RX MEDLINE=83273707; PubMed=6410398;
 RA RA Gon J., Frangione B.;
 RT RT "Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33.";
 RL RL Proc. Natl. Acad. Sci. U.S.A. 80:4337-4341(1983).
 CC CC -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated galactose and isolated from a patient with Waldenstrom's macroglobulinemia.
 DR DR HASP; P80362; IMLL.
 DR DR GO; GO:0005576; C:extracellular; NAS.
 DR DR GO; GO:0005955; P:immune response; NAS.
 DR DR InterPro; IPR00110; Ig-like.
 DR DR InterPro; IPR003596; Ig_V.
 DR DR Pfam; PF00047; Ig; 1.
 DR DR SMART; SM00406; IgV; 1.
 DR DR PROSITE; PSS0835; Ig_LIKE; 1.
 KW KW Direct protein sequencing; Immunoglobulin V region;
 FT FT Monoclonal antibody.
 FT FT DOMAIN 1 23 Framework-1.
 FT FT DOMAIN 24 34 Complementarity-determining-1.
 FT FT DOMAIN 35 49 Framework-2.
 FT FT DOMAIN 50 56 Complementarity-determining-2.
 FT FT DOMAIN 57 88 Framework-3.
 FT FT DOMAIN 89 97 Complementarity-determining-3.
 FT FT DISULFD 23 88 Framework-4.
 FT FT NON TER 108 108 By similarity.
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;
 Query Match 78.5%; Score 441; DB 1; Length 108;
 Best Local Similarity 78.5%; Pred. No. 5.2e-39;
 Matches 84; Conservative 9; Mismatches 14; Indels 0; Gap_B 0;
 QY 1 DIQWQSPSSLSASVGDRVTITCKASODINSLSWFOQPKAKPILYRANRLVGVPS 60
 Db 1 DIQWQSPSSLSASVGDRVTITCKASODINSLSWFOQPKAKPILYRANRLVGVPS 80
 QY 61 RFSGSGSGDVTISQPERPATYCLQDEFP 95
 Db 61 RFSGSGSGDVTISQPERPATYCLQDEFP 107
 RESULT 13
 KV10_HUMAN STANDARD; PRT; 108 AA.
 ID KV10_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-I region Rei.
 OS Homo sapiens (Human).
 OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 OC OC NCBI_TAXID=9606;
 RN RN [1]
 RP RP SEQUENCE.
 RA RA Palm W., Hilzemann N.,
 MEDLINE=76023758; PubMed=809329;

RESULT 12
 KV10_HUMAN

		RESULT 14
RT	"The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Re1); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site."	
RT	Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).	
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).	
RX	MEDLINE=6039368; PubMed=118131;	
RA	EPP O., Hattman E.B., Schiffer M., Huber R., Palm W.; "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein Re1 refined at 2.0-A resolution.", Biochemistry 14:4933-4932(1975).	
RL	--! MISCELLANEOUS: The C region of this chain has the INV (1,2) marker.	
CC	--! MISCELLANEOUS: This is a Bence-Jones protein.	
DR	PIR: A91663; KIHUR3.	
DR	PDB; 1ARZ; X-ray; @E=1-107.	
DR	PDB; 1BWN; X-ray; A/B=1-107.	
DR	PDB; 1REX; X-ray; A/B=1-107.	
DR	GO; GO:0005576; C:extracellular; NAS.	
DR	GO; GO:0003823; F:antigen binding; NAS.	
DR	GO; GO:0006953; IgM; P:immune response; NAS.	
DR	InterPro; IPR00710; Ig-like.	
DR	InterPro; IPR003595; Ig_V.	
DR	PFAM; PF00047; Ig; 1.	
DR	SMART; SM00405; IgV; 1.	
DR	PROSITE; PS50035; Ig_LIKE; 1.	
KW	PD-structure; Bence-Jones protein; direct protein sequencing; Immunoglobulin V region.	
DOMAIN	1 23 Framework-1.	
PT	24 34 Complementarity-determining-1.	
PT	35 49 Framework-2.	
PT	50 56 Complementarity-determining-2.	
PT	57 88 Framework-3.	
PT	89 97 Complementarity-determining-3.	
PT	98 107 Framework-4.	
PT	10 13 STRAND	
PT	14 16 STRAND	
PT	19 25 STRAND	
PT	30 31 TURN	
PT	33 38 STRAND	
PT	40 41 TURN	
PT	45 49 STRAND	
PT	50 52 TURN	
PT	53 54 STRAND	
PT	56 57 TURN	
PT	60 61 STRAND	
PT	62 67 TURN	
PT	68 69 STRAND	
PT	70 75 STRAND	
PT	80 82 HELIX	
PT	84 90 STRAND	
PT	97 98 STRAND	
PT	102 106 STRAND	
SQ	NON_TER 108 108 SEQUENCE 108 AA; 11902 MW; 988143E1188BCE2A CRC64;	
Query Match	78.3%; Score 439; DB 1; Length 108;	
Best Local Similarity	79.2%; Pred. No. 8-4e-38;	
Matches	84; Conservative 6; Mismatches 16; Indels 0; Gaps 0;	
QY	1 DIQWTOQSPSSLSASVGDRVTITCKASODINSYLSWFOOKPGKAKTLYRANLVDGVS	
Db	1 DIQWTOQSPSSLSASVGDRVTITCKASODINSYLSWFOOKPGKAKTLYRANLVDGVS 60	
Qy	61 RPSSGSGGQDYLTISLOPEDFATVYQDQYDEPYTREGGKWEI 106	
61 RPSSGSGGQDYLTISLOPEDFATVYQDQYDEPYTREGGKWEI 106		
Db	61 RPSSGSGGQDYLTISLOPEDFATVYQDQYDEPYTREGGKWEI 129	
	RESULT 15	
QY	1 DIQWTOQSPSSLSASVGDRVTITCKASODINSYLSWFOOKPGKAKTLYRANLVDGVS 60	
Db	23 DIQWTOQSPSSLSASVGDRVTITCKASODINSYLSWFOOKPGKAKTLYRANLVDGVS 82	
QY	61 RPSSGSGGQDYLTISLOPEDFATVYQDQYDEPYTREGGKWEI 107	
Db	83 RFSSGSGGQDYLTISLOPEDFATVYQDQYDEPYTREGGKWEI 129	
Q96SA9		

ID Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TREMBrel. 19, Created)
DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
DB anti-streptococal/anti-myosin immunoglobulin kappa light chain
variable region (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Cetartiodactyla; Homidae; Homo.
OX NCBI_TAXID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson, E. E., Shikloman, A. R., Ward, K. B., Cunningham, M. W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
antibody V region genes." J. Immunol. 161:2020-2031 (1998).
RL EMBL; U96396; ARB6885.1; -.
DR PIR; B49047; BA9047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; IBWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003595; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SW00406; IgV; 1.
DR PROSITE; PS50835; Ig_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
Query Match 77.8%; Score 436.5; DB 2; Length 107;
Matches 87; Conservative 6; Mismatches 13; Indels 1; Caps 1;
OY 1 DIQWTOQSPSSLSASVGDYVITCKASQDINSYISWFQOKRGKPKTLTYRANRNUDGPS 60
Db 1 DIQWTOQSPSSLSASVGDYVITCKASQDINSYISWFQOKRGKPKTLTYRANRNUDGPS 60
OY 61 RFSGSGSGGDDYTITISSIQPEDFATYYCQYDSEPRPYTGGKKEIK 107
Db 61 RFSGSGSGGDDYTITISSIQPEDFATYYC-QSYSTLTFGGKKEIK 106

Search completed: December 29, 2004, 18:05:21
Job time : 73.8584 secs

Copyright GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 29, 2004, 17:46:45 ; Search time 16.323 Seconds
Sequence: 1 EVOLVOSGAEVKRGASKVKT.....GNFPYFYFDYNGQGTLLTVSS 119

Title: US-10-774-076-12
Perfect score: 642

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%;
Listing first 45 summaries

Database : PIR_79,*
1: pir1,*
2: pir2,*
3: pir3,*
4: pir4,*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	467.5	72.8	H32513	Ig heavy chain precursor V region (BxW16) - mouse
2	459.5	71.6	118	Ig heavy chain pre
3	459.5	71.6	119	Ig heavy chain Vr
4	457.5	71.3	128	Ig heavy chain Vr
5	456.5	71.1	150	Ig heavy chain Vr
6	450	70.1	142	Ig heavy chain Vr
7	448.5	69.9	120	Ig heavy chain Vr
8	448.5	69.9	128	Ig heavy chain Vr
9	448.5	69.9	139	Ig heavy chain Vr
10	446	69.5	128	Ig heavy chain Vr
11	445.5	69.5	123	Ig heavy chain Vr
12	445.5	69.4	118	Ig heavy chain Vr
13	445	69.3	119	Ig heavy chain Vr
14	43.5	69.1	116	Ig heavy chain Vr
15	44.3	69.0	117	Ig heavy chain Vr
16	44.3	69.0	121	Ig heavy chain Vr
17	442.5	68.9	124	Ig heavy chain Vr
18	442.5	68.9	135	Ig heavy chain Vr
19	441.5	68.8	117	Ig heavy chain Vr
20	440	68.5	121	Ig heavy chain Vr
21	43.9	68.4	118	Ig heavy chain Vr
22	43.9	68.4	122	Ig heavy chain Vr
23	43.8	68.3	120	Ig heavy chain Vr
24	43.8	68.2	118	Ig heavy chain Vr
25	43.8	68.2	119	Ig heavy chain Vr
26	43.7	68.1	120	Ig heavy chain Vr
27	43.7	68.1	125	Ig heavy chain Vr
28	43.6	67.9	129	Ig heavy chain Vr
29	67.9	133	2	Ig heavy chain Vr

ALIGNMENTS

RESULT 1
H32513
Ig heavy chain precursor V region (BxW16) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: H32513
R;Korller, R.; Strohal, R.S.; Johnson, M.B.; Noonan, D.J.; Duchosal, M.A.,
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Molecule type: DNA
A;Residues: 1-137 <KOF>
A;Cross-references: EMBL:218846; NID:9196949; PID:AA338848.1; PID:9196950
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.8%; Score 467.5; DB 2; Length 137;
Best Local Similarity 73.9%; Pred. No. 8.3e-35;
Matches 88; Conservative 14; Mismatches 15; Indels 1; Gaps 1;

Qy 1 EVOLVOSGAEVKRGASKVKT.....GNFPYFYFDYNGQGTLLTVSS 119
Db 20 BIQLQQSGABLVRKGASKVKT.....GNFPYFYFDYNGQGTLLTVSS 119

Qy 61 SQPFKGAKATLVKSTSTAYMELLSIASEDTAVTYCRRGNPYPYPPWQGQTLTVSS 119
Db 80 NOQPKGKATLTVDKSSTAYMELLSIASEDSAVYCYARK-NYGSFPDWGQGTLLTVSS 137

RESULT 2
S3265

Ig heavy chain V region (clone alpha-MUCL-1) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999

C;Accession: S32625
R;Griffiths, A.D.; Malmqvist, M.; Marke, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty,

EMBO J. 12, 725-734, 1993

A;Title: Human anti-Sm antibodies with high specificity from phage display libraries

A;Reference number: S32625; MUID:93178448; PMID:7679990

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-118 <GR>

A;Cross-references: EMBL:218846; NID:9193121; PID:CA79398.1; PID:9193900

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.6%; Score 459.5; DB 2; Length 118;
Best Local Similarity 73.9%; Pred. No. 3.7e-34;

Matches 88; Conservative 11; Mismatches 19; Indels 1; Gaps 1;

Qy 1 EVOLVOSGAEVKPGASVKISKVSKVSYAFTNNYMWROAPKGKLEWIGYIDPYGDPGY 60

Db 1 QVOLVOSGAEVKPGASVKISKVSKVSYAFTNNYMWROAPKGKLEWIGYIDPYGDPGY 60

Qy 61 SQKFKKATLVDKSTAYMELSSLRSED TAVYCAARRGNFPYFDFWQGQTLVTSS 119

Db 61 AOKFOCKVITRDTSASTAYNELSLRSEDTAVYCA-RDFLSGQYLDWQGQGLTVSS 118

RESULT 3 F30502

Ig heavy chain V region (A52) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000

A;Accession: P30502

R;Bilat., D.; Webster, D.M.; Rees, A.R.

J; Immunol. 141: 1745-1753, 1988

A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice

A;Status: Preliminary

A;Residue: 1-19 <ESTL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 71.6%; Score 439.5; DB 2; length 119;

Matches 88; Conservative 13; Mismatches 14; Indels 7; Gaps 2;

Qy 1 EVOLVOSGAEVKPGASVKISKVSKVSYAFTNNYMWROAPKGKLEWIGYIDPYGDPGY 60

Db 1 BIQLOQSAEVLVKGASVKISKVSKVSYAFTNNYMWROAPKGKLEWIGYIDPYGDPGY 60

Qy 61 SQKFKKATLVDKSTAYMELSSRSRDAVYCA---RRGNFPYFDFWQGQTLVTSS 119

Db 61 NOKFKGKATLTDKSSSTAYMQLNLTSEDSAVYCARGRLLRREG---YFDWQGQTLVT 117

Or 117 VS 118

Db 118 VS 119

RESULT 4 PH0052

Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)

C;Species: Homo sapiens (man)

C;Accession: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

A;Title: Evidence for somatic selection of natural autoantibodies.

A;Reference number: PH0052; MUID:9220280; PMID:152221

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-28 <MAR>

C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>

F;1-30/Region: framework 1

F;15-98/Region: immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;55-67/Region: framework 2

F;68-90/Region: complementarity-determining 2

F;99-116/Region: complementarity-determining 3

Query Match 71.3%; Score 457.5; DB 2; Length 128;

Best Local Similarity 68.0%; Pred. No. 68-34; Matches 87; Conservative 15; Mismatches 17; Indels 9; Gaps 1;

Qy 1 EVOLVOSGAEVKPGASVKISKVSKVSYAFTNNYMWROAPKGKLEWIGYIDPYGDPGY 60

Db 1 QVOLVOSGAEVKPGASVKISKVSKVSYAFTNNYMWROAPKGKLEWIGYIDPYGDPGY 60

Qy 61 SQKFKKATLVDKSTAYMELSSLRSED TAVYCAARRGNFPYFDFWQGQTLVTSS 119

Db 61 AOKFOCKVITRDTSASTAYNELSLRSEDTAVYCA-RDFLSGQYLDWQGQGLTVSS 118

RESULT 5 PNO44

Ig heavy chain V region precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Accession: PNO44 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

R;Kalitz, B.; Betz, G.; Shao, H.; Diamantis, T.; Weidle, U.H.

Gene 122..328 1992

A;Title: A general method for chimerization of monoclonal antibodies by inverse polymer A;Reference number: PNO44; MUID:93138402; PMID:1339379

A;Molecule type: mRNA

A;Residue: 1-150 <KAL>

A;Cross-references: GBIL02346

C;Superfamily: immunoglobulin

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-10/Domain: Ig heavy chain V region #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 74.8%; Pred. No. 8.7e-34;

Matches 89; Conservative 74; Mismatches 21; Indels 1; Gaps 1;

Qy 1 EVOLVOSGAEVKPGASVKISKVSKVSYAFTNNYMWROAPKGKLEWIGYIDPYGDPGY 60

Db 20 EVOLVOSGAEVKPGASVKISKVSKVSYAFTNNYMWROAPKGKLEWIGYIDPYGDPGY 60

Qy 80 NOKFKGKATLTDKSSSTAYMQLNLTSEDSAVYCARGRLLRREG---YFDWQGQTLVT 79

Db 80 NOKFKGKATLTDKSSSTAYMQLNLTSEDTAVYCA-RDFLSGQYLDWQGQGLTVSS 119

RESULT 6 A32483

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Accession: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996

R;Harrick, J.W.; Danielson, L.; Brenner, C.A.; Abramhamson, M.; FTY, K.E.; Borrebaek, C.; Bloch, Biochem. Biophys. Res. Commun. 150:256, 1989

A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells using a reference library.

A;Reference number: A32483; MUID:89273586; PMID:249327

A;Status: preliminary

A;Molecule type: mRNA

A;Residue: 1-142 <AR>

A;Cross-references: GB:M26463

C;Superfamily: heterotetramer; immunoglobulin

C;Keywords: heterotetramer; immunoglobulin

F;25-108/Domain: immunoglobulin homology <IMM>

Query Match 70.1%; Score 450; DB 2; Length 142;

Best Local Similarity 69.3%; Pred. No. 3.1e-33; Matches 88; Conservative 10; Mismatches 21; Indels 8; Gaps 1;

Qy 1 EVOLVOSGAEVKPGASVKISKVSKVSYAFTNNYMWROAPKGKLEWIGYIDPYGDPGY 60

Db 6 VQLQSGPVELVPGASMKLCKTSGTYFTEYMWKQSHGKSLWIGRFNPNGSTYN 65
 Qy 62 QKFKGKATLTVDKSISTAYMELSSRSRSEDTAVYCARGNF----PYFDWQGQTLT 116
 Db 66 QKFKGKATLTVDKSISTAYMELSSRSRSEDTAVYCARGNP--YFDWQGQTLT 125
 Qy 117 VSS 119
 Db 126 VSS 128

RESULT 11
 D33548 Ig heavy chain V-1 region (WIL2) - human
 C;Species: Homo sapiens (man)
 C;Accession: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
 R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
 A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression
 A;Reference number: A33548; MUID:89345575; PMID:2503826
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-123 <KIP>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.5%; Score 446; DB 2; Length 123;
 Best Local Similarity 67.5%; Pred. No. 6.2e-33;
 Matches 83; Conservative 18; MisMatches 18; Indels 4; Gaps 1;

Qy 1 EVOLVQSGAEVKPGASVKISKVSKVSYAFTNMYWQDQPKGKLEWIGYIDPYGDGY 60
 Db 1 QVQLVQSGAEVKPGASVKISKVSKVSYAFTNMYWQDQPKGKLEWIGYIDPYGDGY 60

Qy 61 SOKFKGKATLTVDKSISTAYMELSSRSRSEDTAVYCARRG---NFPYYPDYQGQTLT 116
 Db 61 AEKFQGRVTITRDTTSINTAYMELSLRLSDDTAVYCARASYC3DCCYFPDYQGQTLT 120

Qy 117 VSS 119
 Db 121 VSS 123

RESULT 12
 S38717 Ig heavy chain V region - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
 R;Cimanis, A.Y.
 submitted to the EMBL Data Library, November 1993
 A;Reference number: S38713
 A;Accession: S38717
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-118 <CIM>
 A;Cross-references: EMBL:X76020; NID:9416099; PIDN:CA033607_1; PID:91334262
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 C;Keywords: heterotetramer; immunoglobulin homology <IMM>

Query Match 69.4%; Score 445.5%; DB 2; Length 118;
 Best Local Similarity 72.9%; Pred. No. 6.5e-33;
 Matches 86; Conservative 11; Mismatches 18; Indels 3; Gaps 2;

Qy 3 QLVQSGAEVKPGASVKISKVSKVSYAFTNMYWQDQPKGKLEWIGYIDPYGDGY 60
 Db 3 QLQSGPDLVKPGASVKISKVSKVSYAFTNMYWQDQPKGKLEWIGYIDPYGDGY 62
 Qy 63 KFKGKATLTVDKSISTAYMELSSRSRSEDTAVYCARGN--WFDWQGQTLTVSS 119

Db 63 KFKGKATLTVDKSISTAYMELSSRSRSEDTAVYCARGNP--YFDWQGQTLT 118
 Qy 64 KFKGKATLTVDKSISTAYMELSSRSRSEDTAVYCARGNP--YFDWQGQTLT 118

RESULT 13
 S20640 Ig heavy chain V region - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: S20640; S20644
 R;Lozman, M.; Fasy, T.M.; Novick, K.E.; Monesier, M.
 A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice reacted with the EMBL Data Library, February 1992
 A;Reference number: S20639

A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 1-119 <LOS>
 A;Cross-references: EMBL:X65002; NID:952600; PIDN:CAA46135_1; PID:952601; EMBL:X64999; 1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 C;Keywords: heterotetramer; immunoglobulin homology <IMM>
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.3%; Score 445; DB 2; Length 119;
 Best Local Similarity 70.6%; Pred. No. 7.3e-33;
 Matches 84; Conservative 14; MisMatches 21; Indels 0; Gaps 0;

Qy 1 EVOLVQSGAEVKPGASVKISKVSKVSYAFTNMYWQDQPKGKLEWIGYINPYNDGSKY 60
 Db 1 EVOLVQSGAEVKPGASVKISKVSKVSYAFTNMYWQDQPKGKLEWIGYINPYNDGSKY 60

Qy 61 SOKFKGKATLTVDKSISTAYMELSSRSRSEDTAVYCARRG---NFPYYPDYQGQTLT 119
 Db 61 NEFKGKATLTVDKSISTAYMELSSRSRSEDTAVYCARRG---NFPYYPDYQGQTLT 119

RESULT 14
 PR0959 Ig heavy chain V region (36+ T-L26) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Accession: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 A;Title: Evidence for somatic selection of natural autoantibodies
 A;Reference number: PR0959
 A;Accession: PR0959
 R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-16 <MAR>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 R;Cimanis, A.Y.
 submitted to the EMBL Data Library, November 1993
 A;Reference number: S38713
 A;Accession: S38717
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-118 <CIM>
 A;Cross-references: EMBL:X76020; NID:9416099; PIDN:CA033607_1; PID:91334262
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 C;Keywords: heterotetramer; immunoglobulin homology <IMM>

Query Match 69.1%; Score 443.5%; DB 2; Length 116;
 Best Local Similarity 71.4%; Pred. No. 9.7e-33;
 Matches 85; Conservative 15; MisMatches 16; Indels 3; Gaps 1;

Qy 1 EVOLVQSGAEVKPGASVKISKVSKVSYAFTNMYWQDQPKGKLEWIGYIDPYGDGY 60
 Db 1 QVQLVQSGAEVKPGASVKISKVSKVSYAFTNMYWQDQPKGKLEWIGYIDPYGDGY 60

Qy 61 SOKFKGKATLTVDKSISTAYMELSSRSRSEDTAVYCARRG---WFDWQGQTLTVSS 119
 Db 61 ADKFQGRVTITADESTISTAYMELSSRSRSEDTAVYCARGN--WFDWQGQTLTVSS 119

Search completed: December 29, 2004, 18:06:58
 Job time : 17.497 sec
 Number : 15
 S03305
 Ig heavy chain V region (6B12) - mouse (fragment)
 C-Species: Mus musculus (house mouse)
 C-Date: 30-Sep-1991 #Sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
 C-Accesion: JL0044; S05276; S03305
 R/Van Cleave, V.H.; Naeve, C.W.; Metzger, D.W.
 J. Exp. Med. 167, 1841-1848, 1988
 A;Title: Do antibodies recognize amino acid side chains of protein antigens independent of sequence? - mouse (fragment)
 A;Accession: JL0043; MUID:88258372; PMID:2455014
 A;Molecule type: mRNA
 A;Residues: 1-117 <VAN>
 A;Cross-references: EMBL:X12381
 R;Metzger, D.W.
 submitted to the EMBL Data Library, July 1988
 A;Reference number: S05276
 A;Accession: S05276
 A;Molecule type: mRNA
 A;Residues: 1-116, T, <MET>
 A;Cross-references: EMBL:X12381; NID:952094; PIDN:CAA30939.1; PID:9930170
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 F;15-98/Domain: immunoglobulin homology <IMM>
 Query Match : 69.0%; Score 443; DB 2; Length 117;
 Best Local Similarity : 72.3%; Pred. No. 1.1e-32;
 Matches : 86; Conservative : 10; Mismatches : 21; Indels : 2; Gaps : 1;
 QY 1 EYQVLVQSGAEEVKPGASVKSICKVSGAFTNNWYRQADEGKGLWIGVYDPYDGPY 60
 1 EYQLOQSQSPGAEKGPSVTKMSCKASGIFTDYYINWTKQSIGKSLWIGVYIPNIDAY 60
 QY 61 SOKFKGKATLTVDKSTAYMLLSSRSDETDVYVYCARRGHPPYDYMWSGTLVTVSS 119
 61 SOKFKGKATLTVDKSSSTAYMLRLSTSDDSAVYCARRN --VYFDYMGOGTIIIVSS 117

THIS PAGE BLANK (USPTO)

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

ON protein - protein search, using SW model

Run on: December 29, 2004, 17:38:43 ; Search time 82.1416 Seconds

(without alignments) 833.556 Million cell updates/sec

Title: US-10-774-076-12

Perfect score: 642

Sequence: 1 EVQLVQSGAEVKPGASVKI.....GNFPYFYFDYNGQGTLTVTSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	468	72.9	120	2 Q920E8
2	454	70.7	119	2 Q9UL94
3	450.5	70.2	124	2 Q9UL92
4	449	69.9	464	2 AAH19337
5	448.5	69.9	498	2 Q6N041
6	448.5	69.9	498	2 CAE4829
7	445	69.3	123	2 Q8VJ11
8	445	69.3	146	2 Q924R8
9	441.5	68.8	465	2 Q6PJZ2
10	441.5	68.8	465	2 AAH18280
11	440	68.5	470	2 Q7TMK1
12	439	68.4	472	2 Q6PJZ7
13	439	68.4	472	2 AAH18235
14	439	68.4	472	2 Q9QXFO
15	438	68.2	470	2 AAH62336
16	438	68.2	139	1 HV07_MOUSE
17	433.5	67.5	145	2 Q924Q7
18	433.5	67.5	144	2 Q924P5
19	433	67.4	20	Q924R4
20	432.5	67.4	145	2 AAH37361
21	430.5	67.2	467	1 AAH37361
22	430.5	67.1	145	2 Q924Q6
23	430.5	67.1	145	2 Q924R1
24	430.5	67.1	159	2 Q96Q60
25	429.5	66.9	145	2 Q924Q9
26	429.5	66.9	482	2 Q8K172
27	429.5	66.8	473	2 Q9D8L4
28	428.5	66.7	115	2 Q9UL89
29	428.5	66.7	145	2 Q924P7
30	426.5	66.7	117	1 HV12_MOUSE
31	426.5	66.4	143	2 Q924R0

ALIGNMENTS

RESULT 1		PRELIMINARY		PRT;	120 AA.
ID	Q920E8	AC	Q920E8;	DT	01-DEC-2001 (Tremblrel. 19, Created)
				DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)
				DR	Ptein-imimicking anti-idiotope heavy chain variable region (Fragment).
				DB	Mus musculus (Mouse).
				OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC
				NCBI_TaxID	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NCBI_TaxID=10090;
				RN	[1]
				RA	SEQUENCE FROM N.A.
				RA	Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.; EMBL; AF307936; AAL09420.1; -.
				DR	HSSP; P01751; INQB.
				DR	InterPro; IPR003566; Ig_V.
				DR	PFAM; PF00047; Ig_I.
				DR	PROSITE; PS50835; Ig_LIKE; 1.
				FT	NON_TER 1
				FT	NON_TER 120 120
				SQ	SEQUENCE 120 AA: 13204 MN; DC4834AB1DB56F3C CRC64;
					Query Match 72.9%; Score 468; DB 2; Length 120; Best Local Similarity 75.0%; Pred. No. 1.8e-40; Matches 90; Conservative 10; Mismatches 18; Indels 2; Gaps 1;
					QY
				Db	1 EVQLVQSGAEVKPGASVKIISCKVSGIAFTNTNNWVWQAPGKLEWGYIDYYGDFY 60 1 EVQLVQSGAEVKPGASVKIISCKVSGIAFTNTNNWVWQAPGKLEWGYIDYYGDFY 60
				Db	61 SOKERKGKATLVDKSTTYAMBLSSLRSBDTAVYCA--RRGNPPYFYDYGQOTLVTS 118 61 SOKERKGKATLVDKSTTYAMBLSSLRSBDTAVYCA--RRGNPPYFYDYGQOTLVTS 118
				Db	61 NOKFKGKATLVDKSSRYMQLSLIDESDAVYCAVITYYGNSPAWFAYWGGQTIVTS 120 61 NOKFKGKATLVDKSSRYMQLSLIDESDAVYCAVITYYGNSPAWFAYWGGQTIVTS 120
					RESULT 2
					Q9UL94 PRELIMINARY PRT; 119 AA.
				ID	Q9UL94;
				AC	Q9UL94;
				DT	01-MAY-2000 (Tremblrel. 13, Created)
				DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)
				DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)
				DE	Myelin-reactive immunoglobulin heavy chain variable region (Fragment).
				DE	Homo sapiens (Human).
				OS	Bularycota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC
				NCBI_TaxID	Mammalia; Eutheria; Primates; Cetartiodactyla; Hominidae; Homo; NCBI_TaxID=9606;

RX	MEDLINE=22388257; PubMed=12477932;	RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Scheuer G.D.,	RA	Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,		
RA	Klaunert R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,	RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haien F.,	RA	Krzewinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.B.,		
RA	Diacenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,	RA	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human		
RA	Stapleton M., Bonaldo M.F., Cabavant T.L., Scheetz T.E., Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Louquellone N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunnarine P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzewinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzewinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human	RT	and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RA	Raha S.S., Louquellone N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunnarine P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzewinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human	RN	[2]		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzewinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human	RP	SEQUENCE FROM N.A.		
RC	Strains=Czech II; Tissue=My mammary tumor;	RC	TISSUE=My mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.		
RC	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.	RC	Expression driven by an MMV-LTR enhancer.;		
RA	Strausberg R.	RA	Strausberg R.		
RA	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.	RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.		
RA	EMBL: BC055910; AMH55910.1; -.	DR	EMBL: BC055910; AMH55910.1; -.		
RA	InterPro: IPR003597; Ig_c1.	DR	InterPro: IPR003597; Ig_c1.		
RA	InterPro: IPR003006; Ig_MHC.	DR	InterPro: IPR003006; Ig_MHC.		
RA	InterPro: IPR003596; Ig_v.	DR	InterPro: IPR003596; Ig_v.		
RA	Pfam: PF07654; Cl-set; 3.	DR	Pfam: PF07654; Cl-set; 3.		
RC	PROSITE; PS00047; Ig_1.	DR	PROSITE; PS00047; Ig_1.		
RA	PROSITE; PS50835; Ig_LIKE; 4.	DR	PROSITE; PS50835; Ig_LIKE; 4.		
DR	KW	KW	Hypothetical protein.		
RA	SEQUENCE 465 AA; 51329 MW; 394F43C4B8DB3B21 CRC64;	SQ	SEQUENCE 470 AA; 51727 MW; 6D90B4DP896BB090 CRC64;		
RESULT 11		Query, Match, Best local similarity 68.9%; Score 441.5; DB 2; Length 465; Matches 84; Conservative 12; Mismatches 20; Indels 3; Gaps 1;	Query, Match, Best local similarity 68.5%; Score 440; DB 2; Length 470; Matches 86; Conservative 13; Mismatches 19; Indels 4; Gaps 2;		
Q7MKL	PRELIMINARY;	PRT; 470 AA.	Q7MKL	PRELIMINARY;	PRT; 470 AA.
ID	Q7MKL		ID	Q7MKL	
AC	Q7MKL;		AC	Q7MKL;	
DT	01-OCT-2003 (Tremblrel. 25, Created)		DT	01-OCT-2003 (Tremblrel. 25, Last sequence update)	
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)		DT	01-OCT-2003 (Tremblrel. 25, Last sequence update)	
DE	Hypothetical protein AI324045.		DE	Hypothetical protein AI324045.	
GN			GN		
OS	Mus musculus (Mouse)		OS	Mus musculus (Mouse)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;		OX	NCBI_TaxID=10090;	
RN	SEQUENCE FROM N.A.		RN	SEQUENCE FROM N.A.	
RR	STRAIN=CZECH II;		RR	STRAIN=CZECH II;	
RC	TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR enhancer.;		RC	TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR enhancer.;	
RX	MEDLINE=22388257; PubMed=12477932;		RX	MEDLINE=22388257; PubMed=12477932;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Scheuer G.D.,		RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Scheuer G.D.,	
RA	Klaunert R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,		RA	Klaunert R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Bluetow K.H., Schaefer C.F., Bhat N.K.,		RA	Altschul S.F., Zeeberg B., Bluetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F., Diachenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E., Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Louquellone N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunnarine P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzewinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human		RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzewinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzewinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human		RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzewinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human	
RA	Strausberg R.,		RA	Strausberg R.	
RA	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.		RA	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.	
RA	EMBL: BC055910; AMH55910.1; -.		RA	EMBL: BC055910; AMH55910.1; -.	
RA	InterPro: IPR003597; Ig_c1.		RA	InterPro: IPR003597; Ig_c1.	
RA	InterPro: IPR003006; Ig_MHC.		RA	InterPro: IPR003006; Ig_MHC.	
RA	InterPro: IPR003596; Ig_v.		RA	InterPro: IPR003596; Ig_v.	
RA	Pfam: PF07654; Cl-set; 3.		RA	Pfam: PF07654; Cl-set; 3.	
RC	PROSITE; PS00047; Ig_1.		RC	PROSITE; PS00047; Ig_1.	
RA	PROSITE; PS50835; Ig_LIKE; 4.		RA	PROSITE; PS50835; Ig_LIKE; 4.	
RA	KW		RA	KW	
RA	Hypothetical protein.		RA	Hypothetical protein.	
RA	SEQUENCE 465 AA; 51329 MW; 394F43C4B8DB3B21 CRC64;		RA	SEQUENCE 470 AA; 51727 MW; 6D90B4DP896BB090 CRC64;	
RESULT 12		Query, Match, Best local similarity 68.5%; Score 440; DB 2; Length 470; Matches 86; Conservative 13; Mismatches 19; Indels 4; Gaps 2;	RESULT 12		Query, Match, Best local similarity 68.5%; Score 440; DB 2; Length 470; Matches 86; Conservative 13; Mismatches 19; Indels 4; Gaps 2;
Q9GZ2	PRELIMINARY;	PRT; 119 AA.	Q9GZ2	PRELIMINARY;	PRT; 119 AA.
ID	Q9GZ2;		ID	Q9GZ2;	
AC	Q9GZ2;		AC	Q9GZ2;	
DT	01-MAR-2001 (Tremblrel. 15, Created)		DT	01-MAR-2001 (Tremblrel. 15, Last sequence update)	
DT	01-MAR-2001 (Tremblrel. 15, Last annotation update)		DT	01-MAR-2001 (Tremblrel. 15, Last sequence update)	
DE	Monoclonal antibody NP30 heavy chain variable region (Fragment).		DE	Monoclonal antibody NP30 heavy chain variable region (Fragment).	
GN			GN		
OS	Schistosoma japonicum (Blood fluke); Trematoda: Digenea; Strigeida; Schistosomatidae; Schistosomatidae; Schistosoma.		OS	Schistosoma japonicum (Blood fluke); Trematoda: Digenea; Strigeida; Schistosomatidae; Schistosomatidae; Schistosoma.	
OC	Schistosoma japonicum (Blood fluke); Trematoda: Digenea; Strigeida; Schistosomatidae; Schistosomatidae; Schistosoma.		OC	Schistosoma japonicum (Blood fluke); Trematoda: Digenea; Strigeida; Schistosomatidae; Schistosomatidae; Schistosoma.	
OX	Schistosoma japonicum (Blood fluke); Trematoda: Digenea; Strigeida; Schistosomatidae; Schistosomatidae; Schistosoma.		OX	Schistosoma japonicum (Blood fluke); Trematoda: Digenea; Strigeida; Schistosomatidae; Schistosomatidae; Schistosoma.	
RN	[1]		RN	[1]	
RR	SEQUENCE FROM N.A.		RR	SEQUENCE FROM N.A.	
RA	Song X.T., Feng Z.Q., Guan X.H.;		RA	Song X.T., Feng Z.Q., Guan X.H.;	
RA	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.		RA	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.	
RA	EMBL: AR282622; ARG01452.1; -.		RA	EMBL: AR282622; ARG01452.1; -.	
RA	HSSP: P01751; IAGW.		RA	HSSP: P01751; IAGW.	
RA	InterPro: IPR007110; Ig-like.		RA	InterPro: IPR007110; Ig-like.	
RA	InterPro: IPR003596; Ig_v.		RA	InterPro: IPR003596; Ig_v.	
RA	InterPro: IPR00047; Ig_1.		RA	InterPro: IPR00047; Ig_1.	
RA	PROSITE; PS00046; Ig_v.		RA	PROSITE; PS00046; Ig_v.	
RA	PROSITE; PS50835; Ig_LIKE; 1.		RA	PROSITE; PS50835; Ig_LIKE; 1.	
RA	NON_TER 1		RA	NON_TER 1	
RA	SEQUENCE 119 AA; 13567 MW; BA893873FD5PA6AB CRC64;		RA	SEQUENCE 119 AA; 13567 MW; BA893873FD5PA6AB CRC64;	

Query Match	68.4%	Score 439;	DB 2;	Length 119;
Best Local Similarity	69.7%	Pred. No.	1. 8e-37;	
Matches	83;	Conservative	12;	Mismatches 24; Indels 0; Gaps 0;
Ov	1	EYOLVQSGAEVKPGASVVKISKVSKVGYAFTNMYWVROAQPKGLEWIGYIDPYGDPY	60	
Db	1	EVOLVQSGAEVKPGASVVKISKVSKVGYAFTNMYWVROAQPKGLEWIGYIDPYGDPY	60	
Ov	61	SQEKKGATLVDKSSTAYMELSSLRSEDTAVYCARNSCAGTTFCTYMMWVROAQPKGLEWIGYINPSRGTY	119	
Db	61	NQEKKGATLVDKSSTAYMELSSLRSEDTAVYCARNSCAGTTFCTYMMWVROAQPKGLEWIGYINPSRGTY	119	
RESULT 13				
O6PJA7				
ID O6PJA7		PRELIMINARY;	PRT;	472 AA.
AC Q6PJA7;				
DT 05-JUL-2004 (TRIMBREL. 27, Last sequence update)				
DT 05-JUL-2004 (TRIMBREL. 27, Last annotation update)				
DE Hypothetical protein.				
OS Mus musculus (Mouse).				
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX NCBI_TaxID=10090;				
RN [1]				
SEQUENCE FROM N.A.				
RC STRAIN=Czech II;				
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.				
RC Expression driven by an MMTV-LTR enhancer.;				
RX MEDLINE=22388257; PubMed=1477932;				
RA Strauberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.,				
RA Klausner R.D., Collins F.S., Wagner L., Sheinmen C.M., Schuler G.D.,				
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blatt N.K.,				
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA Diatchenko L., Marszina K., Farmer A.A., Rubin G.M., Hong L.,				
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,				
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E.,				
RA Jones S.J., Marra M.A., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,				
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RT "Generation and initial analysis of more than 15,000 full-length human				
RT and mouse cDNA sequences.",				
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				
RN [2]				
SEQUENCE FROM N.A.				
RC STRAIN=Czech II;				
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.				
RC Expression driven by an MMTV-LTR enhancer.;				
RA Strauberg R.,				
RA Submitted (DIC-2001) to the EMBL/GenBank/DBJ databases.				
DR EMBL; BC018535; AAH1835.1; -.				
DR InterPro; IPR00359; Ig-like.				
DR InterPro; IPR007110; Ig-cl.				
DR InterPro; IPR00306; Ig_MHC.				
DR InterPro; IPR003396; Ig_v.				
PFam; PF07654; Cl-set; 3.				
DR InterPro; IPR00359; Ig-like.				
DR SMART; SW00409; Ig; 2.				
DR SMART; SW00407; IgCl; 3.				
DR SMART; SW00405; IgV; 1.				
DR PROSITE; PS00835; Ig_LIKE; 4.				
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.				
KW Hypothetical protein.				
RESULT 14				
O6PJA7				
ID O6PJA7		PRELIMINARY;	PRT;	472 AA.
AC Q6PJA7;				
DT 02-MAR-2004 (TRIMBREL. 27, Last sequence update)				
DT 02-MAR-2004 (TRIMBREL. 27, Last annotation update)				
DE Hypothetical protein.				
OS Mus musculus (Mouse).				
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX NCBI_TaxID=10090;				
RN [1]				
SEQUENCE FROM N.A.				
RC STRAIN=Czech II; TISSUE=Mammary tumor;				
RX MEDLINE=22388257; PubMed=12477932;				
RA Strauberg R.D.; Feingold E.A.; Grouse L.H.; Derge J.G.,				
RA Klausner R.D., Collins F.S., Wagner L., Sheinmen C.M., Schuler G.D.,				
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blatt N.K.,				
RA Diatchenko L., Marszina K., Farmer A.A., Rubin G.M., Hong L.,				
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,				
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E.,				
RA Jones S.J., Marra M.A., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,				
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RT "Generation and initial analysis of more than 15,000 full-length human				
RT and mouse cDNA sequences.",				
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				
RN [2]				
SEQUENCE FROM N.A.				
RC STRAIN=Czech II; TISSUE=Mammary tumor;				
RA Strauberg R.,				
RA Submitted (DIC-2001) to the EMBL/GenBank/DBJ databases.				
DR EMBL; BC018535; AAH1835.1; -.				
DR InterPro; IPR007110; Ig-like.				
DR InterPro; IPR00359; Ig-cl.				
DR InterPro; IPR00306; Ig_MHC.				
DR InterPro; IPR003396; Ig_v.				
PFam; PF07654; Cl-set; 3.				
DR InterPro; IPR00359; Ig-like.				
DR SMART; SW00409; Ig; 2.				
DR SMART; SW00407; IgCl; 3.				
DR SMART; SW00405; IgV; 1.				
DR PROSITE; PS00835; Ig_LIKE; 4.				
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.				
KW Hypothetical protein.				
SQ SEQUENCE	472 AA;	52299 MW;	165169C23D55D4AB CRC64;	
Query Match	68.4%	Score 439;	DB 2;	Length 472;
Best Local Similarity	69.1%	Pred. No.	8. 5e-37;	
Matches	85;	Conservative	14;	Mismatches 20; Indels 4; Gaps 1;
Ov	1	EYOLVQSGAEVKPGASVVKISKVSKVGYAFTNMYWVROAQPKGLEWIGYIDPYGDPY	60	
Db	20	EVOLVQSGPELVLKVGASVRSMSCKASGYTFSDYMMHWVHQSHGKSLIEWIGVYPNGNGNY	79	
Ov	61	SQEKKGATLVDKSSTAYMELSSLRSEDTAVYCARNSCAGTTFCTYMMWVROAQPKGLEWIGYINPSRGTY	119	
Db	80	NQEKKGATLVDKSSTAYMELSSLRSEDTAVYCARNSCAGTTFCTYMMWVROAQPKGLEWIGYINPSRGTY	119	
Ov	117	VSS 119		
Db	140	VSS 142		
Query Match	68.4%	Score 439;	DB 2;	Length 119;
Best Local Similarity	69.1%	Pred. No.	8. 5e-37;	
Matches	85;	Conservative	14;	Mismatches 20; Indels 4; Gaps 1;
Ov	1	EYOLVQSGAEVKPGASVVKISKVSKVGYAFTNMYWVROAQPKGLEWIGYIDPYGDPY	60	
Db	20	EVOLVQSGPELVLKVGASVRSMSCKASGYTFSDYMMHWVHQSHGKSLIEWIGVYPNGNGNY	79	
Ov	61	SQEKKGATLVDKSSTAYMELSSLRSEDTAVYCARNSCAGTTFCTYMMWVROAQPKGLEWIGYINPSRGTY	119	
Db	80	NQEKKGATLVDKSSTAYMELSSLRSEDTAVYCARNSCAGTTFCTYMMWVROAQPKGLEWIGYINPSRGTY	119	
Ov	117	VSS 119		
Db	140	VSS 142		

us-10-774-076-12.rup

גָּדְעָן וְעַמְּלֵךְ כָּל־עֲמָדָה וְבָרֶכֶת בְּנֵי־יִשְׂרָאֵל

Qy	117	VSS	119
Db	140	VSS	142

RESULT 15 Q9QXF0

AC
PT
Q9QXF0;
01 MVV-2000 (T=EMR1=1) 13 Smart3

DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukarya; Metazoa; Chordata; Craniata; Vertebrata.

OC
OX

[1] SEQUENCE FROM N.A.
Clemens A., Rademaeckers A., Specht C., Koelsch B.:
KN
RP
RA

RL Submitted (DEC-1997) to the ENBL/GenBank/DDBJ database
DR EMBL; AJ225171; CAB65236.1; -.
DP ,
DB ,
LA ,
RE ,

DR InterPro; IPR0031596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM000406; IgV_1.

DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
TM 115 115
VN-TER

NON_IER SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 68.2%; **Score** 438; **DB** 2; **Length** 117;
Best Local Similarity 71.4%; **Pred.** No. 2. **2e-37**; **Marschner et al. Conservative** 13; **Miamarche et al.** 10; **Tadeja et al.** 2; **Same** 1.

Dy 60 95. 27. Jahr 1911

Db 1 EVQLOQSGPELVKPGASVKSCKASGYFTDYMKWVKOSHGSLEWIGDINPNNGGTSY 60

61 NURKENGNAU VUSSSIAMUJNLSUSAVIYCAR--DRUYFYDUMQGUTIVSS 11/

Search completed: December 29, 2004, 18:05:21
Job time : 83.1416 SECs

THIS PAGE BLANK (use

The invention relates to a gene recombinant antibody that has specific reaction with human vascular endothelial growth factor (VEGF) receptor Flt-1. The antibodies are useful for diagnosis and as remedies for diseases due to abnormal neovascularization such as proliferation or metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic retinopathy, premature retinopathy and priories.

Sequence 136 AA;

Query Match	78.5%	Score	504	DB	3	Length	136
Best Local Similarity	80.7%	Pred. No.	1	-7e-36			
Matches	96	Conservative	9	Mismatches	12	Indels	2
Gaps							
1	EVOLVOSCAEVKPGASKISKVGASYGFTNMYWQRDPKGLEWIGYIDPYGGDPSY	60					
20	QVOLVQSCAEVKPGASGVKVSCKASGYTFINNHWRQAGQGLEWMGAIFFGNGFTSY	79					
61	SQKFKGKATLTDKSTTAYMLISSRSEDTAVYCARRGRNPFYFDYNGQTLTVSS	119					
80	NOKFKGRVTITVKSTTAYMELSSLRSEDIVAVYICARDGD-YFDFWQSGTLVTVSS	136					

RESULT 6
AB78865
AB78865 standard; protein; 136 AA.

AAB78865;

20-APR-2001 (first entry)

Anti-human Flt-1 antibody VH CDR protein sequence SEQ ID 87.

Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer; vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody; delayed hypersensitivity; malignant tumour; arteriosclerosis; antibody; synthetic.

WO200079275-A1.

28-DEC-2000.

16-JUN-2000; 2000W0-JP003957.

17-JUN-1999; 99JJP-00171709.

(KROW) KYOWA HAKKO KOGYO KK.

Shittara K, Shibuya M;

WPI; 2001-080847/09.

Substances binding to human vascular endothelial growth factor receptor Flt-1, used for diagnosis and treatment of inflammatory diseases, arteriosclerosis, cancer and delayed hypersensitivity.

Example 3; Page 155, 164pp; Japanese.

This invention relates to a reagent for detecting differentiation of monocytes and macrophages from haematopoietic stem cells, containing a substance which binds to human vascular endothelial growth factor (VEGF) receptor Flt-1. The invention also includes a method for diagnosing a disease in which the differentiation of monocytes and macrophages is implicated, using the reagent, and an agent for the treatment of diseases diagnosed using the method, containing a substance which binds to Flt-1 or a substance which inhibits the signal transduction of Flt-1. Diseases which may be diagnosed or treated include inflammation, delayed hypersensitivity, malignant tumours and arteriosclerosis. AAF70190 - AAF70244, AAF70251 and AAF70258 represent DNA sequences encoding anti-human Flt-1 monoclonal antibody fragments, and oligonucleotides used in the construction of the antibody. The monoclonal antibody is used in the reagent of the invention. PCR primers AAF70245 - AAF7870 (excluding AAF70551) are used in the isolation of the antibody DNA sequences.

CC	Protein sequences AAB78848 - AAB78870 represent fragments of the anti-
CC	human Flt-1 antibody
XX	Sequence 136 AA;
SQ	
Query Match	78.5%; Score 504; DB 4; Length 136;
Best Local Similarity	80.7%; Pred. No. 1.7e-56;
Matches	96; Conservative 9; Mismatches 12; Indels 2; Gaps 1;
OY	1 EYVOLVOSGAEVKRGPKASVSKISKVSKVAFVNMMWYRQAPKGLENIGVYDIPYGPQGY 60
Db	20 QYVOLVOSGAEVKRGPKASVSKISKVSKVSKASGYTFINTVMHWYRQAPCGLEMGAFPQNGPTSY 79
OY	61 SQKPKGKATLTDKSTSTAYMELSLRSEDTAVYCARSGNIFPPYFDYWQGQTLVTSS 119
Db	80 NQKPKGSRVITVDKSTSTAYMELSLRSEDTAVYCARSGNIFPPYFDYWQGQTLVTSS 136
RESULT 7	
AAW84099	ID AAW84099 standard; protein; 110 AA.
XX	AAW84099;
XX	15-MAR-1999 (First entry)
DT	Vitronectin alpha- ν beta-3 Mab VH.
DE	Humanised antibody; monoclonal antibody'; Mab; antibody' engineering; mouse; human; vitronectin; alpha- ν beta-3'; receptor; restenosis; cancer; metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoporosis; Paget's disease; hyperparathyroidism; hypercalcemia; therapy; immunotherapy.
KW	XX
Mus sp.	
XX	
PN	W09840488-A1.
XX	
PD	17-SEP-1998.
XX	
PF	12-MAR-1998; 98W0-US004987.
XX	
PR	12-MAR-1997; 97W5-00395609P.
XX	
PA	(SMK) SMITHKLINE BEECHAM CORP.
XX	
PI	Jonak ZL, Johanson KO, Taylor AH;
XX	
DR	WPI; 1999-034590/03..
DR	N-PSSB; AAV1801.
XX	
PT	New anti alpha- ν beta-3 vitronectin receptor antibodies - used for immunotherapy treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or osteoporosis.
XX	
PS	Example 13; Page 63; 97pp; English.
XX	
CC	This is the amino acid sequence of the region of the murine monoclonal antibody (mAb) D12 heavy chain variable region (VH) that is altered in humanised D12 VH (see also AAW84097). A synthetic gene (see AAV1801) encoding the protein was prepared from synthetic oligonucleotides and used to prepare an expression vector for humanised D12 VH. D12 is an antibody for passive immunotherapy of disorders mediated by the alpha- ν beta-3 vitronectin receptor, e.g. restenosis and angiogenic associated diseases
CC	
SQ	Sequence 110 AA;

CC	caused the production of the antibody from the hybridoma cell line.
CC	(updated on 25-MAR-2003 to correct PN field.)
XX	Sequence 135 AA;
SQ	Query Match 77.5%; Score 497.5'; DB 2; Length 135; Best Local Similarity 79.0%; Pred. No. 6.2e-36; Indels 3; Gaps 1; Matches 94; Conservative 11; Mismatches 11;
QY	1 EWLQVSGARWKKGASVSKISKVSGAFTINNNWVRQAPKGLEWIGYIDPYGGPSQ 62
DB	1 OLVQSGAETVKKGASVSKSGAFTISINNNWVRQAPQGLEMIGYADPYGGPSQ 60
Db	63 KFKGKATLTVDKS1STAYMELSSLRSEDATAVYVCCR--GNFPYFDDYNGQTL 114
QY	61 RPKGKATLTVDKS1STAYMELSSLRSEDATAVYVCCR--GNFPYFDDYNGQTL 110
CC	RESULT 8
CC	ID AR29017
CC	ID AR29017 standard; protein; 135 AA.
AC	AAR29017;
KW	25-MAR-2003 (revised)
DT	30-MAR-1993 (first entry)
XX	pUC-RVh-1220d.
XX	Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse; monoclonal; hybridoma; PCR; plasmid; polymerase chain reaction; amplification.
XX	Synthetic.
XX	Location/Qualifiers
PH	1..19
FT	peptide /note= "Leader peptide"
FT	Region 20..49
FT	/label= FR1
FT	Region 50..54
FT	/label= CDR1
FT	Region 55..68
FT	/label= FR2
FT	Region 69..85
FT	/label= CDR2
FT	Region 86..117
FT	/label= FR3
FT	Region 118..124
FT	/label= CDR3
FT	Region 125..135
FT	/label= PR4
XX	W09219759-A1.
XX	12-NOV-1992.
XX	24-APR-1992;
PP	92WO-JP00544.
PR	25-APR-1991; 91JP-00095476.
PR	19-FEB-1992; 92JP-00032084.
XX	(CHUS) CHUGAI SEIYAKU KK.
XX	Tsuchiya M, Sato K, Bendig MM, Jones ST, Saldanha JW;
DR	WPI; 1992-398882/48.
DR	N-PSDB; AAQ01391.
XX	The sequences given in AR29016-17 are portions of monoclonal antibodies which were encoded by plasmids contained within the mouse hybridoma, AUK12-20. The DNA encoding the complementarity determining regions (CDR's) was isolated by polymerase chain reaction. These antibodies recognise human interleukin-6 receptor (IL-6R). The hybridoma cells were transformed with plasmids containing fragments of the antibody gene which
CC	Reconstituted human antibody to human interleukin-6 receptor - has low antigenicity and contains mouse V-region complementarity determining regions.
PR	Disclosure; Page 159-60; 207pp; Japanese.
XX	The sequences given in AR29016-17 are portions of monoclonal antibodies which were encoded by plasmids contained within the mouse hybridoma, AUK12-20. The DNA encoding the complementarity determining regions (CDR's) was isolated by polymerase chain reaction. These antibodies recognise human interleukin-6 receptor (IL-6R). The hybridoma cells were transformed with plasmids containing fragments of the antibody gene which
CC	caused the production of the antibody from the hybridoma cell line.
CC	(updated on 25-MAR-2003 to correct PN field.)
XX	Sequence 135 AA;
SQ	Query Match 77.5%; Score 497.5'; DB 2; Length 135; Best Local Similarity 79.0%; Pred. No. 6.2e-36; Indels 3; Gaps 1; Matches 94; Conservative 11; Mismatches 11;
QY	1 EWLQVSGARWKKGASVSKISKVSGAFTINNNWVRQAPKGLEWIGYIDPYGGPSQ 62
DB	1 OLVQSGAETVKKGASVSKSGAFTISINNNWVRQAPQGLEMIGYADPYGGPSQ 60
QY	20 QWLQVSGARWKKGASVSKSGAFTISINNNWVRQAPQGLEMIGYIDPYGGPSQ 79
DB	61 SOKPGKATLTVDKS1STAYMELSSLRSEDATAVYVCCRGNFPYFDDYNGQTLVSS 119
QY	80 NQKEKGKVMTNDISTINAYMELSSLRSEDATAVYVARGGN--RFAYNGQGTIVTUVSS 135
XX	RESULT 9
XX	AAW22418
ID	AAW22418 standard; protein; 116 AA.
XX	AAW22418;
AC	AAC22418;
XX	08-DEC-1997 (first entry)
XX	Reshaped human AUK12-20 VH.
XX	Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy; AUK12-20.
XX	Homo; sapiens.
OS	OS Synthetic.
XX	Chimeric.
XX	Location/Qualifiers
PH	1..30
FT	Region /label= FR1
FT	Region 31..35
FT	/label= CDR1
FT	Region 36..49
FT	/label= FR2
FT	Region 50..66
FT	/label= CDR2
FT	Region 67..98
FT	/label= FR3
FT	Region 99..105
FT	/label= CDR3
FT	Region 106..116
FT	/label= FR4
XX	W09718938-A1.
XX	21-NOV-1995;
XX	95US-00561521.
PR	21-MAY-1997.
PR	21-NOV-1996;
PR	96WO-US018807.
XX	21-NOV-1995; 95US-00561521.
XX	PR (ATHB-) ATHENA NEUROSCIENCES INC.
XX	PT Bendig MM, Leger OJ, Saldanha J, Jones ST, Yednock TA;
XX	DR WPI; 1997-227879/27.
XX	PT Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.
XX	PS Example 6; Page 44; 107pp; English.

XX
 CC This polypeptide comprises version 'b', of a reshaped human antibody
 CC AUK12-20 VH region. A DNA fragment encoding the polypeptide was subcloned
 CC into vector PUC19 for use as a template for PCR amplification and
 CC production of version 'a' of a reshaped human 21.6 VH region (see
 CC AAW22413) that can be used in the construction of novel humanised anti-
 alpha-4 integrin antibodies. Claimed humanised antibodies are useful in
 the treatment of asthma, atherosclerosis, AIDS, dementia, diabetes,
 inflammatory bowel disease, rheumatoid arthritis, transplant rejection,
 graft versus host disease, tumour metastasis, nephritis, aortic
 dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated
 lung injury.

XX SQ Sequence 116 AA;

Query Match 77.3%; Score 496.5; DB 2; Length 116;
 Best Local Similarity 78.2%; Pred. No. 6.6e-36; Mismatches 93; Conservative 12; Indels 11; Gaps 3; PT PT
 Matches 1; PT PT
 Qy 1 EVOLVSGAETVKPGASVKSCSKVSGYAFFNNMWRQAPGKGLEWVGYIDPYGDDG 60
 Db 1 QVOLVSGAETVKPGASVKSCSKVSGYAFFNNMWRQAPGQLEWVGYIDPFGGSIY 60

Qy 61 SQKFKGATLVDKSTSTAYNELLSSRLSRSEDIVAVYCARGEN--RFAYWGQGLTVSS 119
 Db 61 NQKFKGKVMTVDTSINTAYNELLSSRLSRSEDIVAVYCARGEN--RFAYWGQGLTVSS 116

RESULT 10

AAR29016

ID AAR29016 standard; protein; 135 AA.

XX AC

XX DT 25-MAR-2003 (revised)

DT 30-MAR-1993 (first entry)

XX DE pUC-RVh-1220b.

XX KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse; polymerase chain reaction; amplify.

XX OS Synthetic.

XX KEY Location/Qualifiers

PT Peptide 1..19 /note= "Leader peptide"

FT Region 20..49 /label= FR1

FT Region 50..54 /label= CDR1

FT Region 55..68 /label= FR2

FT Region 69..85 /label= CDR2

FT Region 86..117 /label= FR3

FT Region 118..124 /label= CDR3

FT Region 125..135 /label= FR4

XX DR WPI: 1998-575904/49.

XX DR N-PSDB; NAV08097.

XX PT A human type complementarity determining region transplanted antibody
 PT against ganglioside GM2 - useful as an anti-tumour agent and as a
 PT diagnostic for related cancers.

XX PS Example 4; Page 46-47; 66pp; Japanese.

XX CC This sequence is a fragment of an antibody of the invention. The antibody
 CC of the invention is a human complementarity determining region
 transplanted antibody that reacts specifically with ganglioside GM2. DNA

XX PI Tsuchiya M, Sato K, Bendig MM, Jones ST, Saldanha JW;
 XX DR WPI; 1992-39882/48.
 CC DR N-PSDB; AAQ31391.

XX PT Reconstituted human antibody to human interleukin-6 receptor - has low
 PT antigenicity and contains mouse V-region complementarily determining
 PT regions.

XX PS Disclosure; Page 157-8; 207pp; Japanese.

XX CC The sequences given in AAR29016-17 are portions of monoclonal antibodies
 CC which were encoded by plasmids contained within the mouse hybridoma,
 CC AUK12-20. The DNA encoding the complementarity determining regions
 CC (CDR's) was isolated by polymerase chain reaction. These antibodies
 recognise human interleukin-6 receptor (IL-6R). The hybridoma cells were
 CC transformed with plasmids containing fragments of the antibody gene which
 CC caused the production of the antibody from the hybridoma cell line.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 135 AA;

Query Match 77.3%; Score 496.5; DB 2; Length 135;
 Best Local Similarity 78.2%; Pred. No. 7.6e-36; Mismatches 93; Conservative 12; Indels 11; Gaps 3; PT PT
 Matches 1; PT PT
 Qy 1 EVOLVSGAETVKPGASVKSCSKVSGYAFFNNMWRQAPGKGLEWVGYIDPYGDDG 60
 Db 20 QVOLVSGAETVKPGASVKSCSKVSGYAFFNNMWRQAPGQLEWVGYIDPFGGSIY 79

Qy 61 SQKFKGATLVDKSTSTAYNELLSSRLSRSEDIVAVYCARGEN--RFAYWGQGLTVSS 119
 Db 80 NQKFKGKVMTVDTSINTAYNELLSSRLSRSEDIVAVYCARGEN--RFAYWGQGLTVSS 135

RESULT 11

AAW73187

ID AAW73187 standard; protein; 144 AA.

XX AC

XX DT 22-JAN-1999. (first entry)

XX DE Fragment of ganglioside GM2 targeting antibody.

XX KW Ganglioside GM2; antibody; complementarity determining region; cancer;
 KW anti-tumour agent.

XX OS Homo sapiens.

XX FN JP10257893-A.

XX PD 29-SEP-1998.

XX PR 19-MAR-1997; 97JP-00066901.

XX PR 19-MAR-1997; 97JP-00066901.

XX PA (KYOU) KYOWA HAKKO KOGYO KK.

XX DR WPI: 1998-575904/49.

XX DR N-PSDB; NAV08097.

XX PT A human type complementarity determining region transplanted antibody
 PT against ganglioside GM2 - useful as an anti-tumour agent and as a
 PT diagnostic for related cancers.

XX PS Example 4; Page 46-47; 66pp; Japanese.

XX CC This sequence is a fragment of an antibody of the invention. The antibody
 CC of the invention is a human complementarity determining region
 transplanted antibody that reacts specifically with ganglioside GM2. DNA

encoding the antibody, and vectors and transformants containing it, can be used for the recombinant production of the antibody. The antibody itself can be used as an anti-tumour agent or as a diagnostic tool for related cancers. The antibody has anticancer activity against ganglioside GM2 positive cells.

SQ Sequence 144 AA;

Query Match 76.7%; Score 492.5; DB 2; Length 144;

Best Local Similarity 80.0%; Pred. No. 1.8e-35; Matches 96; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 1 EVOLVOSGAEVKKGASVKISKVSGYAFINNMWVRQAPGKLEWIGYIDPYGDPY 60

Db 20 EVOLVOSGAEVKKGASVKISKVSGYAFINNMWVRQAPGKLEWIGYIDPYGDPY 79

QY 61 SOKFKGKATIVDKSTSTAYNELLSSRSDDTAVYCCARRGNPPYIDPYGQGLTVVSS 119

Db 80 NOKFKSKATIVDKSTSTAYNELLSSRSDDTAVYCCARRGNPPYIDPYGQGLTVVSS 139

RESULT 12
ADL11893 ID ADL11893 standard; peptide; 117 AA.
XX AC ADL11893;
XX DT 06-MAY-2004 (first entry)
XX DB CDR transplant antibody heavy chain variable region #4.
XX KW cancer metastasis; human vascular endothelial growth factor; VEGFR;
XX receptor Flt-1; Cyostatic; lung cancer; CDR.
XX OS Homo sapiens.
XX PN JP2003261460-A.
XX PD 16-SEP-2003.
XX PR 08-MAR-2002; 2002JP-00063835.
XX PT 08-MAR-2002; 2002JP-00063835.
XX PA (KYOU) KYOWA HAKKO KOGYO KK.
XX DR N-PSDB; AA287778.
XX PS WPI; 2000-072431/06.
XX PT N-PSDB; AA287778.
XX PT Gene recombinant antibodies, useful for diagnosis and as remedies for diseases due to abnormal neovascularization e.g. proliferation or metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy and psoriasis.
XX PT Claim 28, Page 203, 210pp; Japanese.
XX CC The invention relates to a gene recombinant antibody that has specific reaction with human vascular endothelial growth factor (VEGF) receptor Flt-1. The antibodies are useful for diagnosis and as remedies for diseases due to abnormal neovascularisation such as proliferation or metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic retinopathy, premature retinopathy and psoriasis.
XX SQ Sequence 136 AA;

Query Match 76.6%; Score 492; DB 3; Length 136;

Best Local Similarity 78.2%; Pred. No. 1.9e-35; Matches 93; Conservative 11; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVOLVOSGAEVKKGASVKISKVSGYAFINNMWVRQAPGKLEWIGYIDPYGDPY 60

Db 20 EVOLVOSGAEVKKGASVKISKVSGYAFINNMWVRQAPGKLEWIGYIDPYGDPY 79

QY 61 SOKFKGKATIVDKSTSTAYNELLSSRSDDTAVYCCARRGNPPYIDPYGQGLTVVSS 119

Db 80 NOKFKSKATIVDKSTSTAYNELLSSRSDDTAVYCCARRGNPPYIDPYGQGLTVVSS 136

RESULT 13
ID AAY77600 standard; peptide; 136 AA.
XX AC AAY77600;
XX DT 08-MAY-2000 (first entry)
XX DE Anti-human VEGF receptor Flt-1 antibody related peptide sequence #95.
XX KW Antibody; human; vascular endothelial growth factor; VEGF receptor; Flt-1; neovascularisation; cell proliferation; metastasis; tumour; rheumatoid arthritis; retinopathy; psoriasis.
XX OS Mus musculus.
XX PN WO9960025-A1.
XX PD 25-NOV-1999.
XX PP 20-MAY-1999; 99W0-JP002661.
XX PR 20-MAY-1998; 98JP-00139000.
XX PA (KYOU) KYOWA HAKKO KOGYO KK.
XX PI Shitara K, Ito M, Kawada Y, Nakamura K;
XX DR WPI; 2000-072431/06.
XX PT N-PSDB; AA287778.
XX PT Gene recombinant antibodies, useful for diagnosis and as remedies for diseases due to abnormal neovascularization e.g. proliferation or metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy and psoriasis.
XX PT Claim 28, Page 203, 210pp; Japanese.
XX CC The invention relates to a gene recombinant antibody that has specific reaction with human vascular endothelial growth factor (VEGF) receptor Flt-1. The antibodies are useful for diagnosis and as remedies for diseases due to abnormal neovascularisation such as proliferation or metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic retinopathy, premature retinopathy and psoriasis.
XX SQ Sequence 136 AA;

Query Match 76.6%; Score 492; DB 3; Length 136;

Best Local Similarity 78.2%; Pred. No. 1.9e-35; Matches 93; Conservative 11; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVOLVOSGAEVKKGASVKISKVSGYAFINNMWVRQAPGKLEWIGYIDPYGDPY 60

Db 20 EVOLVOSGAEVKKGASVKISKVSGYAFINNMWVRQAPGKLEWIGYIDPYGDPY 79

QY 61 SOKFKGKATIVDKSTSTAYNELLSSRSDDTAVYCCARRGNPPYIDPYGQGLTVVSS 119

Db 80 NOKFKSKATIVDKSTSTAYNELLSSRSDDTAVYCCARRGNPPYIDPYGQGLTVVSS 136

Query Match 76.6%; Score 492; DB 8; Length 117;

Best Local Similarity 78.2%; Pred. No. 1.6e-35; Matches 93; Conservative 11; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVOLVOSGAEVKKGASVKISKVSGYAFINNMWVRQAPGKLEWIGYIDPYGDPY 60

Db 1 QVQVQSGAVVKKGASVKISKVSGYTFNNMWWVRQAPGKLEWIGAIPENGTSY 60

DE Anti-human Flt-1 antibody VH CDR protein sequence SEQ ID 91.
 XX
 KW Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer;
 KW vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody;
 KW delayed hypersensitivity; malignant tumour; arteriosclerosis.
 OS Synthetic.
 XX
 PN WO200079275-A1.
 XX
 PD 28-DEC-2000.
 XX
 PP 16-JUN-2000; 2000WO-JP003357.
 XX
 PR 17-JUN-1999; 99JP-00171709.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Shitara K, Shibuya M;
 XX
 DR WPI; 2001-080847/09.
 XX
 N-PSDB; AAF70251.
 XX
 PT Substances binding to human vascular endothelial growth factor receptor
 PT Flt-1, used for diagnosis and treatment of inflammatory diseases,
 PT arteriosclerosis, cancer and delayed hypersensitivity.
 XX
 PS Example 3, Page 15-158; 164pp; Japanese.
 XX
 CC This invention relates to a reagent for detecting differentiation of
 CC monocytes and macrophages from haematopoietic stem cells, containing a
 CC substance which binds to human vascular endothelial growth factor (VEGF)
 CC receptor Flt-1. The invention also includes a method for diagnosing a
 CC disease in which the differentiation of monocytes and macrophages is
 CC implicated, using the reagent, and an agent for the treatment of diseases
 CC diagnosed using the method, containing a substance which binds to Flt-1
 CC or a substance which inhibits the signal transduction of Flt-1. Diseases
 CC which may be diagnosed or treated include inflammation, delayed
 CC hypersensitivity, malignant tumours and arteriosclerosis. AAF10190 -
 CC AAF0244, AAF0251 and AAF70258 represent DNA sequences encoding anti-
 CC human Flt-1 monoclonal antibody fragments, and oligonucleotides used in
 CC the construction of the antibody. The monoclonal antibody is used in the
 CC reagent of the invention. PCR primers AAF70245 - AAF70246 (excluding
 CC AAF0251) are used in the isolation of the antibody DNA sequences.
 CC Protein sequences AAB78848 - AAB78870 represent fragments of the anti-
 CC human Flt-1 antibody
 XX
 Sequence 136 AA;

Query Match 76.6%; Score 422; DB 4; Length 136;
 Best Local Similarity 78.2%; Pred. No. 1.9e-35;
 Matches 93; Conservative 11; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVQLVQSGAEVKKGAVKISKVSKVSGVFTNYNMYWROAKGKGLEIGYDPYGDGY 60
 Db 20 QVQLVQSGAEVKKGAVKISKVSKVSGVFTNYNMYWROAKGKGLEIGYDPYGDGY 79
 QY 61 SOKFKGKALTVDKSTAYMELSSLASEDTAVYCARRGHPYDYGCGTIVVS 119
 Db 80 NOKFKGKALTVDKSTAYMQLRSLSRSDTAVYFCARDG--YVFDYWGCGTIVVS 136
 RESULT 15
 AAB0795
 ID AAB0795 standard; protein; 135 AA.
 XX
 AC AAB0795;
 XX
 DT 14-NOV-2000 (first entry)
 DE A heavy chain variable region of humanised 3D1 antibody.
 XX
 KW Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;

KW autoimmune disease; infectious disease; inflammatory disorder;
 KW systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;
 KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
 KW multiple sclerosis; transplant rejection; proliferative disease;
 KW leukemia; anaemia; sickle-cell anaemia; thalassemia;
 KW aplastic anaemia; myeloid dysplasia syndrome.
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.

XX
 PH Key location/Qualifiers
 PT Peptide 1..19
 PT /note= "signal peptide"
 PT Protein 20..135
 PT /note= "mature protein"
 PT Region 50..54
 PT /note= "complementarity determining region 1"
 PT Region 69..85
 PT /note= "complementarity determining region 2"
 PT Region 118..124
 PT /note= "complementarity determining region 3"
 XX
 PN WO20047625-A2.
 XX
 PD 17-AUG-2000.
 XX
 PP 09-FEB-2000; 2000WO-US0033303.
 XX
 PR 12-FEB-1999; 99US-00249011.
 XX
 PR 24-JUN-1999; 99US-00339596.
 PA (GEMY) GENETICS INST INC.
 XX
 PI Co MS, Vasquez M, Carrasco B, Celinker AC, Collins M, Goldman S;
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
 XX
 DR WPI; 2000-524532/47.
 XX
 N-PSDB; AAS59594.

PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecule,
 PT modulates immune responses and can therefore treat e.g. autoimmune
 PT diseases, infectious diseases.

XX
 PS Example 3, Fig 2A; 162pp; English.

XX
 CC The present sequence represents the heavy chain variable region of the
 CC humanised murine antibody 3D1. The antibody has a binding specificity to
 CC B7 molecules. The antibody is used to construct humanized
 CC immunoglobulins, which comprise an antigen binding region of non-human
 CC origin and a portion of a human immunoglobulin. The humanized
 CC immunoglobulins are useful for treating autoimmune diseases, infectious
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,
 CC also useful for treating a transplant recipient or preventing transplant
 CC rejection in a transplant recipient, and treating proliferative disease
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome
 XX
 Sequence 135 AA;

Query Match 76.4%; Score 490.5; DB 3; Length 135;
 Best Local Similarity 78.2%; Pred. No. 2.6e-35;
 Matches 93; Conservative 11; Mismatches 12; Indels 3; Gaps 1;

QY 1 EVQLVQSGAEVKKGAVKISKVSKVSGVFTNYNMYWROAKGKGLEIGYDPYGDGY 60
 Db 20 QVQLVQSGAEVKKGAVKISKVSKVSGVFTNYNMYWROAKGKGLEIGYDPYGDGY 79
 QY 61 SOKFKGKALTVDKSTAYMELSSLASEDTAVYCARRGHPYDYGCGTIVVS 119

Mon Jan 3 13:38:47 2005

us-10-774-076-12.rag

Page 9

Db :|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
80 NQKPERKGATMVDKSTTAYNMLSSLRSEDATVYCARA--WYMDYNGQGTUVSS 135

Search completed: December 29, 2004, 17:57:34
Job time : 83.796 secs

THIS PAGE BLANK (USPTO)

US-10-774-076-17
; Sequence 17, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design labs, Inc.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882-0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
; US-10-774-076-17
Query Match 100.0%; Score 642; DB 17; Length 138;
Best Local Similarity 100.0%; Pred. No. 1e-51; Mismatches 0; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EVOLVOSGAEVKKGASVKISCKSVKSGYAFNTNMWVROAQPKGLEWIGVYDGY 60
Db 20 EVOLVOSGAEVKKGASVKISCKSVKSGYAFNTNMWVROAQPKGLEWIGVYDGY 79
Qy 61 SOKFKGKATLTVDKSSTAYMELESLRSEDTAVYVCCRGNFPYFYDYGQGTIVSS 119
Db 80 SOKFKGKATLTVDKSSTAYMELESLRSEDTAVYVCCRGNFPYFYDYGQGTIVSS 138
RESULT 3
US-10-774-076-2
; Sequence 2, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882-0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: mus sp.
; US-10-774-076-2
Query Match 87.9%; Score 554; DB 17; length 119;
Best Local Similarity 84.9%; Pred. No. 1.4e-44; Mismatches 9; Indels 0; Gaps 0;
Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
Qy 1 EVOLVOSGAEVKKGASVKISCKSVKSGYAFNTNMWVROAQPKGLEWIGVYDGY 60
Db 1 EVOLVOSGAEVKKGASVKISCKSVKSGYAFNTNMWVROAQPKGLEWIGVYDGY 60
Qy 61 SOKFKGKATLTVDKSSTAYMELESLRSEDTAVYVCCRGNFPYFYDYGQGTIVSS 119
Db 61 SOKFKGKATLTVDKSSTAYMELESLRSEDTAVYVCCRGNFPYFYDYGQGTIVSS 119
RESULT 4
US-10-774-076-9
; Sequence 9, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.

RESULT 5
US-10-223-880-5
; Sequence 5, Application US/10223-880
; Publication No. US20030152571A1
; GENERAL INFORMATION:
; APPLICANT: JONAK, ZDENKA
; APPLICANT: JOHANSSON, KIUNG O.
; APPLICANT: TAYLOR, ALEXANDER
; TITLE OF INVENTION: ANIT-ALPHABETA3 HUMANIZED MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: P5-0629C1
; CURRENT APPLICATION NUMBER: US/10/223,880
; PRIOR APPLICATION NUMBER: 09/380,910
; PRIOR FILING DATE: 1999-05-10
; PRIOR APPLICATION NUMBER: PCT/US98/04987
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/039,609
; PRIOR FILING DATE: 1997-03-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-223-880-5
Query Match 82.6%; Score 530; DB 14; Length 117;
Best Local Similarity 85.1%; Pred. No. 1.9e-41; Mismatches 7; Indels 6; Gaps 2;
Matches 103; Conservative 7; Mismatches 7; Indels 6; Gaps 2;
Qy 1 EVOLVOSGAEVKKGASVKISCKSVKSGYAFNTNMWVROAQPKGLEWIGVYDGY 60
Db 1 EVOLVOSGAEVKKGASVKISCKSVKSGYAFNTNMWVROAQPKGLEWIGVYDGY 60
Qy 61 SOKFKGKATLTVDKSSTAYMELESLRSEDTAVYVCCRGNFPYFYDYGQGTIVSS 118
Db 61 SOKFKGKATLTVDKSSTAYMELESLRSEDTAVYVCCRGNFPYFYDYGQGTIVSS 116
Qy 119 S 119
Db 117 S 117
RESULT 6
US-10-160-232-91

Sequence 91, Application US/10160232
 Publication No. US20030088075A1
 GENERAL INFORMATION:
 APPLICANT: SHITARA, KENYA
 APPLICANT: ITO, MIKITO
 APPLICANT: HANAI, NOBUO
 APPLICANT: NAKAMURA, KAZUYASU
 TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOClonAL ANTIBODY
 FILE REFERENCE: 249-107
 CURRENT APPLICATION NUMBER: US/10/160,232
 CURRENT FILING DATE: 2002-06-04
 PRIOR APPLICATION NUMBER: US/09/453,718
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: 9/315,051
 PRIOR FILING DATE: 1999-05-20
 PRIOR APPLICATION NUMBER: 09/119,014
 PRIOR FILING DATE: 1998-07-20
 PRIOR APPLICATION NUMBER: PCT/JP97/04259
 PRIOR FILING DATE: 1997-11-21
 NUMBER OF SEQ ID NOS: 96
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 91
 LENGTH: 136
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
 US-10-160-232-91

Query Match 78.5%; Score 504; DB 14; Length 136;
 Best Local Similarity 80.7%; Pred No. 5.8e-39; Mismatches 12; Indels 2; Gaps 1;
 Matches 96; Conservative 9; Nucleotide 0.

QY 1 EVOLVOSGAEVKPGASVKISCKSGYAFNTNNWQRQAPGKLEMGIVDYPYGDGY 60
 Db 20 QVOLVQSGAVKPGASVKISCKSGYAFNTNNWQRQAPGKLEMGIVDYPYGDGY 79

QY 61 SOKPKGKATLVDKSTAYMELSSRSIDTAVYCARRGNFPYFDWGGQGLVTSS 119
 Db 80 NOKEKGKVITVTDKSTAYMELSSRSIDTAVYCARRGNFPYFDWGGQGLVTSS 135

RESULT 7
 US-10-223-880-12 Application US/10223880
 ; Sequence 12, Application US/10223880
 ; Publication No. US2003012571A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JONAK, ZDENKA
 ; APPLICANT: JOHNSON, KYUNG O.
 ; APPLICANT: TAYLOR, ALEXANDER
 ; TITLE OF INVENTION: ANTI-ALPHABETA3 HUMANIZED MONOClonAL
 ; FILE REFERENCE: P5029C1
 ; CURRENT APPLICATION NUMBER: US/10/223,880
 ; CURRENT FILING DATE: 2002-08-20
 ; PRIOR APPLICATION NUMBER: 09/380,910
 ; PRIOR FILING DATE: 1999-09-10
 ; PRIOR APPLICATION NUMBER: PCT/US98/04987
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/039,609
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 12
 ; LENGTH: 110
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-10-223-880-12

Query Match 78.3%; Score 503; DB 14; Length 110;
 Best Local Similarity 85.1%; Pred. No. 5.8e-39;

Matches 97; Conservative 6; Mismatches 5; Indels 6; Gaps 2;
 US-10-160-232-95
 ; Sequence 95, Application US/10160232
 ; Publication No. US20030088075A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SHITARA, KENYA
 ; APPLICANT: ITO, MIKITO
 ; APPLICANT: HANAI, NOBUO
 ; APPLICANT: NAKAMURA, KAZUYASU
 ; APPLICANT: SHIBUYA, MASABUMI
 ; APPLICANT: NAKAMURA, KAZUYASU
 ; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOClonAL ANTIBODY
 ; FILE REFERENCE: 249-107
 ; CURRENT APPLICATION NUMBER: US/10/160,232
 ; CURRENT FILING DATE: 2002-06-04
 ; PRIOR APPLICATION NUMBER: US/09/453,718
 ; PRIOR FILING DATE: 1999-12-03
 ; PRIOR APPLICATION NUMBER: 9/315,051
 ; PRIOR FILING DATE: 1998-05-20
 ; PRIOR APPLICATION NUMBER: 09/119,014
 ; SEQ ID NO: 95
 ; LENGTH: 136
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
 US-10-160-232-95

Query Match 76.6%; Score 492; DB 14; Length 136;
 Best Local Similarity 78.2%; Pred. No. 7.5e-38; Mismatches 11; Indels 2; Gaps 1;
 Matches 93; Conservative 11; Nucleotide 0.

QY 1 EVOLVOSGAEVKPGASVKISCKSGYAFNTNNWQRQAPGKLEMGIVDYPYGDGY 60
 Db 20 QVOLVQSGAVKPGASVKISCKSGYAFNTNNWQRQAPGKLEMGIVDYPYGDGY 79

QY 61 SOKPKGKATLVDKSTAYMELSSRSIDTAVYCARRGNFPYFDWGGQGLVTSS 119
 Db 80 NOKEKGKVITVTDKSTAYMELSSRSIDTAVYCARRGNFPYFDWGGQGLVTSS 135

RESULT 9
 US-09-249-011A-6
 ; Sequence 6, Application US/09249011A
 ; Patent No. US20020116855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CO, MAN SUNG
 ; APPLICANT: VASQUEZ, MAXIMILIANO
 ; APPLICANT: CARRERO, BEATRIZ
 ; APPLICANT: CHENIKER, ARBIE CHERYL
 ; APPLICANT: COLLINS, MARY
 ; APPLICANT: GOLDMAN, SAMUEL
 ; APPLICANT: GRAY, GARY S.
 ; APPLICANT: KNIGHT, ANDREA
 ; APPLICANT: O'HARA, DENISE
 ; APPLICANT: RUPP, BONITA
 ; APPLICANT: VELDMAN, GEBRTRUIDA M.

; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702_0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Humanized
; FEATURE:
; OTHER INFORMATION: murine anti-human B7-2 heavy chain
; US-09-249-011A-6

Query Match 76.4%; Score 490.5; DB 9; Length 135;
Best Local Similarity 78.2%; Pred. No. 1e-37; Indels 3; Gaps 1;
Matches 93; Conservative 11; Mismatches 12; Indels 3; Gaps 1;
QY 1 EVOLVOSGAEVKPGASVKISKVSKYGAFFNNMMWQRQPKGLEWIGYIDPYGGDY 60
Db 20 QVOLVQSGAEVKPGSSVKVSKYGAFTDYNHWWQRQPKGLEWIGYIYPNGGGY 79

QY 61 SQKFKGKATIVDKSTSTAYMELSLRSEDTAVYCARRGNFIFYFDWQGQLVTSS 119
Db 80 NQKPKGKATIVDKSTSTAYMELSLRSEDTAVYCAR--WMDYWGQGLVTSS 135

RESULT 10
US-09-249-011A-24
Sequence 24 Application US/09249011A
; Patent No. US20001765531
; GENERAL INFORMATION:
; APPLICANT: CO., MAN, SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRERO, BEATRIZ
; APPLICANT: CEUNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOODMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702_0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Mus sp.

; US-09-249-011A-24

Query Match 76.4%; Score 490.5; DB 9; Length 461;
Best Local Similarity 78.2%; Pred. No. 3.7e-37;
Matches 93; Conservative 11; Mismatches 12; Indels 3; Gaps 1;

QY 1 EVOLVOSGAEVKPGASVKISKVSKYGAFFNNMMWQRQPKGLEWIGYIDPYGGDY 60
Db 20 QVOLVQSGAEVKPGSSVKVSKYGAFTDYNHWWQRQPKGLEWIGYIYPNGGGY 79

QY 61 SQKFKGKATIVDKSTSTAYMELSLRSEDTAVYCARRGNFIFYFDWQGQLVTSS 119
Db 80 NQKPKGKATIVDKSTSTAYMELSLRSEDTAVYCAR--WMDYWGQGLVTSS 135

RESULT 12
US-10-389-155-16
; Sequence 16 Application US/0389155
; Publication No. US20030229208A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; Co. Man Sung
; Schneider, William P.
; Landolfi, Nicholas F.
; Coeligh, Kathleen L.
; Selick, Harold E.
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/389,155
; FILING DATE: 13-Mar-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,000
; FILING DATE: 01-JUN-1999
; APPLICATION NUMBER: US 07/229,975
; FILING DATE: 28-DEC-1988
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 08/484,537
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30-223
; REFERENCE/DOCKET NUMBER: 011823-002650US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; STRANEDNESS: <Unknown>
; MOLECULE TYPE: linear
; TOPOLGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
; US-10-389-155-16

Query Match 76.1%; Score 488.5; DB 14; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-37;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVOLVOSGAEVKPGASVKISKVSKYGAFFNNMMWQRQPKGLEWIGYIDPYGGDY 60
Db 1 QVOLVQSGAEVKPGSSVKVSKYGAFTDYNHWWQRQPKGLEWIGYIYPNGGGY 60

QY 61 SQKFKGKATIVDKSTSTAYMELSLRSEDTAVYCARRGNFIFYFDWQGQLVTSS 119
Db 61 NQKPKGKATIVDKSTSTAYMELSLRSEDTAVYCAR--GRP-AMDYWGQGLVTSS 116

RESULT 12
US-10-389-417-16
; Sequence 16 Application US/10389417
; Publication No. US20040049014A1

GENERAL INFORMATION:

APPLICANT: Queen, Cary L.

Co., Man Sung

Schneider, William P.

Landolfi, Nicholas F.

Coelingh, Kathleen L.

Selick, Harold E.

TITLE OF INVENTION: Improved Humanized Immunoglobulins

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/389,417

FILING DATE: 13-Mar-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/325,000

FILING DATE: 01-JUN-1999

APPLICATION NUMBER: US/07/290,975

FILING DATE: 28-DEC-1988

APPLICATION NUMBER: US/07/310,252

FILING DATE: 13-FEB-1989

APPLICATION NUMBER: US/07/590,274

FILING DATE: 28-SEP-1990

APPLICATION NUMBER: US/07/634,278

FILING DATE: 19-DEC-1990

APPLICATION NUMBER: US/08/484,537

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30-223

REFERENCE DOCKET NUMBER: 011823-002650US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULAR TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-10-389-417-16

Query Match 76.1%; Score 488.5; DB 15; Length 116;
 Best Local Similarity 79.0%; Pred. No. 1.3e-37;
 Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVQLVQSGAELVKKGASVKSICKVSKVSGYAFFNNKMYWVQGPKGKLEWGVYIDPYVGDSY 60
 :|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

RESULT 13

US-10-412-357-57

Sequence 57, Application US/10452357

Publication No. US2004005414A1

GENERAL INFORMATION:

US-10-148-844-43

Query Match 75.8%; Score 486.5; DB 14; Length 118;

Best Local Similarity 77.9%; Prod. No. 2.1e-37;

Matches 95; Conservative 7; Mismatches 13; Indels 7; Gaps 2;

SEQUENCE DESCRIPTION: SEQ ID NO 43

RESULT 14

US-10-148-844-43

Query Match 75.8%; Score 486.5; DB 14; Length 118;

Best Local Similarity 77.9%; Prod. No. 2.1e-37;

Matches 95; Conservative 7; Mismatches 13; Indels 7; Gaps 2;

SEQUENCE DESCRIPTION: SEQ ID NO 43

RESULT 15

US-10-148-844-43

Query Match 75.8%; Score 486.5; DB 14; Length 118;

Best Local Similarity 77.9%; Prod. No. 2.1e-37;

Matches 95; Conservative 7; Mismatches 13; Indels 7; Gaps 2;

SEQUENCE DESCRIPTION: SEQ ID NO 43

RESULT 15
 US-10-127-890-169
 ; Sequence 169, Application US/10127890
 ; Publication No. US20030166196A1
 ; GENERAL INFORMATION:
 ;
 APPLICANT: Better, Marc D.
 ;
 Carroll, Stephen F.
 STUDNIKA, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 Proteins
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US10/127,890
 FILING DATE: 23-Apr-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US10/646,360
 FILING DATE: 13-May-1996
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-May-1994
 APPLICATION NUMBER: US08/064,691
 FILING DATE: 12-May-1993
 APPLICATION NUMBER: US07/988,430
 FILING DATE: 09-Dec-1992
 APPLICATION NUMBER: US07/901,707
 FILING DATE: 19-Jun-1992
 APPLICATION NUMBER: US07/787,567
 FILING DATE: 04-Nov-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEX: 650-398-1248
 TELEFAX: 312/707-9155
 INFORMATION FOR SEQ ID NO: 169:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 169:
 US-10-127-890-169

Job time : 68.8024 Secs

Query Match 75.3%; Score 483.5; DB 14; Length 116;
 Best Local Similarity 77.3%; Pred. No. 3; ge-37;
 Matches 92; Conservative 11; Mismatches 13; Indels 3; Gaps 1;

Qy 1 EVOLVOSGAEVKPGASVKSCKVSGYAFINNMWVROAPGKLEWIGWIDPYGDPGV 60
 Db 1 EVOLVOSGAEVKPGASVKSCKVSGYAFINNMWVROAPGKLEWIGWIDPYGDPGV 60
 Qy 61 SOKFKGKATLTVDKSTSTAMELSLRSEDTAVYCARRNPPYFD---YWGGTLYTV 117
 Db 61 SOKFKGKATLTVDKSTSTAMELSLRSEDTAVYCARRNPPYFD---YWGGTLYTV 117
 Qy 118 SS 119
 Db 117 SS 118

Qy 1 EVOLVOSGAEVKPGASVKSCKVSGYAFINNMWVROAPGKLEWIGWIDPYGDPGV 60
 Db 1 EVOLVOSGAEVKPGASVKSCKVSGYAFINNMWVROAPGKLEWIGWIDPYGDPGV 60
 Qy 61 SOKFKGKATLTVDKSTSTAMELSLRSEDTAVYCARRNPPYFD---YWGGTLYTV 119
 Db 61 SOKFKGKATLTVDKSTSTAMELSLRSEDTAVYCARRNPPYFD---YWGGTLYTV 119
 Qy 61 NOKPKDATTADESTNTAMELSLRSEDTAVYCARRG--VFDYWGGTLYTV 116
 Db 61 NOKPKDATTADESTNTAMELSLRSEDTAVYCARRG--VFDYWGGTLYTV 116

Copyright GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:37:57 ; Search time 75.6047 Seconds
521.928 Million cell updates/sec

Title: US-10-774-076-5
Perfect score: 576
Sequence: 1 QAVVTDQSLALTNSPGFVTL..... ALWYSHHWWFGGGTKTIVLG 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_GeneSeq_23Sep04:*

- 1: geneseqdp1980b:*
- 2: geneseqdp1990b:*
- 3: geneseqdp2000b:*
- 4: geneseqdp2016:*
- 5: geneseqdp2002b:*
- 6: geneseqdp2003b:*
- 7: geneseqdp2003b:*
- 8: geneseqdp2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	RESULT
1	559	97.0	112	AAR89720	1 AAR89720
2	559	97.0	269	AAR54756	ID AAR89720 standard; protein; 112 AA.
3	559	97.0	415	AAR56484	XX AC
4	556	96.5	269	AAR56482	XX AAR89720;
5	555	96.4	131	AAR03422	XX DT
6	555	96.4	131	AAR06211	XX 26-SBP-1996 (first entry)
7	555	96.4	131	AAR85058	XX DE
8	555	96.4	131	AABU8892	XX Mouse antibody lambda chain variable region consensus sequence.
9	553	96.0	114	ADM07541	XX KW Antibody; stability; instability; mutagenesis; amino acid frequency.
10	553	96.0	128	AAR95949	XX KW canonical sequence approximation; substitution; immunoglobulin;
11	550	95.5	112	AAY03868	XX KW light chain; variable region; VL-region; diagnosis; immunoassay;
12	548	95.1	261	AAY44990	XX KW cancer treatment; autoimmune disease; immunotoxin; improved yield.
13	547	95.0	229	ADM07542	XX OS Mus musculus.
14	547	95.0	229	ADM07544	XX PN
15	95.0	229	7	ADM07543	XX PD
16	546	94.8	214	ADM07541	XX 18-JAN-1994; 94DB-04425115.
17	546	94.8	256	AAR22568	XX PR
18	546	94.8	256	AAR22582	XX (BOPP) BOERINGER MANNHEIM GMBH.
19	546	94.8	428	ADM07542	XX PT Steipe B, Steinbacher S;
20	546	94.8	443	ADM07544	XX DR WPI; 1996-069594/08.
21	94.6	402	2	AAR24025	XX PS
22	542	94.1	256	AAR2584	XX Functional antibodies modified to increase or decrease stability - have
23	541	93.9	110	AAR05038	XX PT specific amino acid substns. In the variable domain, determined by
24	541	93.9	110	AAR5136	XX PT reference to consensus sequences.
25	541	93.9	272	ADE29203	XX XX XX

Claim 2; Page 35; 43pp; German.

Consensus sequences were established for antibody variable regions from human and mouse heavy and light (kappa and lambda) chains. In addition, frequency tables listing the amino acids which can be found at each position were compiled. In a new method, mutations are introduced into an antibody variable domain by reference to the frequency table. When an amino acid is replaced by one which occurs at a higher frequency at that position, the resulting antibody chain is more stable than the wild-type; when an amino acid is replaced by one which occurs less frequently (or not at all), the resulting antibody is less stable than the wild-type. Stabilised antibodies are useful as diagnostic reagents, as catalysts and in treatment of cancer, autoimmune diseases and infections. Destabilised

CC antibodies have improved (faster) pharmacokinetic properties. The present
CC sequence is the mouse lambda light chain variable region consensus.
XX

SQ Sequence 112 AA;

Query Match 97.0%; Score 559; DB 2; Length 112;
Best Local Similarity 97.3%; Pred. No. 1.2e-39; Indels 0; Gaps 0;
Matches 107; Conservative 0; Mismatches 3; OS

Qy 1 QAVVTOBSALTTSPGETVTTCRSTGAVTTSNANWVKPDLFTLIGGTRNRYVGV 60
Db 1 QAVVTOBSALTTSPGETVTTCRSTGAVTTSNANWVKPDLFTLIGGTRNRYVGV 60
Qy 61 PARFSGSLIGDKAALTTGAQTEDAIYCALWYSNHWVFGGGKLTVLG 110
Db 61 PARFSGSLIGDKAALTTGAQTEDAIYCALWYSNHWVFGGGKLTVLG 110

RESULT 2

AARS4756

ID AARS4756 standard; protein; 269 AA.

AC AARS4756;

XX

DT 25-MAR-2003 (revised)
06-DEC-1994 (first entry)

XX DE PRAS11 between HindIII and EcoRI sites.

XX KW Single chain Fv fragment; ScFv; Gene Therapy; Adenovirus; penton fibre; Ads; Fusion sites; PCR; Polymerase chain reaction.

OS Synthetic.

XX

FH Key Location/qualifiers

FT Protein 1: .269

FT Peptide /label= Single chain Fv fragment
1: .22

FT Protein /label= pELB leader peptide
23: .142

FT Region /label= heavy chain variable region
23: .51

FT Region /label= VH FRI
52: .57

FT Region /label= VH CDR 1
58: .71

FT Region /label= VH FR2
72: .88

FT Region /label= VH CDR 2
89: .120

FT Region /label= VH FR3
121: .131

FT Region /label= VH CDR 3
132: .142

FT Peptide /label= VH FRI
143: .265

FT Protein /label= (G48)3 Linker
158: .269

FT Region /label= Light chain variable region
158: .179

FT Region /label= VL FRI
180: .193

FT Region /label= VL CDR 1
194: .207

FT Region /label= VL FRI
208: .215

FT Region /label= VL CDR 2
216: .247

FT Region /label= VL FRI
248: .256

FT Region /label= VL CDR 3
257: .269

FT

XX

PN

XX

PD

XX

PF

XX

PR

XX

PA

XX

PI

XX

DR

XX

N-PSDB

XX

PT

XX

PS

XX

CC

/label= VL FR3

RESULT 3

FT

XX

PN

XX

PD

XX

PF

XX

PR

XX

PA

XX

PI

XX

DR

XX

N-PSDB

XX

PT

XX

PS

XX

CC

OS

Synthetic.

XX

WO-415644-A1.

XX

PD

XX

21-JUL-1994.

XX

Amplification; single chain variable region fusion protein; PCR.

XX

OS

Synthetic.

XX

17-JAN-1994.

XX

94WO-GB000087..

XX

15-JAN-1993;

PR

93GB-0000686.

XX

PA

(IMCR) IMPERIAL CANCER RESEARCH TECHNOLOGY.

XX

PI	Epenetos AA, Spooner RA, Deonarin M;
DR	WPI; 1994-24807/30.
XX	N-PSDB; AAQ70660.
PT	New cpds. comprising a targetting portion and a cytotoxic portion - used esp. for treating mammals for destroying target cells, partic. tumour cells.
PT	Disclosure; Fig 10; 114pp; English.
CC	The sequence is that of the ScFv PRAS109 and PRAS113 between HindIII and EcoRI site obt'd. by PCR. See also AAR56482-5. (Updated on 25-MAR-2003 to correct PN field.)
CC	Sequence 415 AA;
XX	Query Match 97.0%; Score 559; DB 2; Length 415; Best Local Similarity 97.3%; Pred. No. 5e-39; 3; Indels 0; Gaps 0; Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 QAVVTOESALTTSPGTVTLCRCSRSTGAVTTSNSANWQEKPDHLFTGLIGGTINRVPGV
Db	158 QAVVTOESALTTSPGTVTLCRCSRSTGAVTTSNSANWQEKPDHLFTGLIGGTINRVPGV 217
Qy	61 PARFGSLIGDKAALTITGAQTEDRAIYFCALWNSNHWVGGGTKLTVLG 110
Db	218 PARFGSLIGDKAALTITGAQTEDRAIYFCALWNSNHWVGGGTKLTVLG 267
RESULT 4	
AAR56482	
ID	AARS6482 standard; protein; 269 AA.
XX	
AC	AAR09422;
XX	
DT	25-MAR-2003 (revised) 04-MAR-1993 (first entry)
DE	Br-3 Light Chain V Region (mouse).
XX	
KW	Monoclonal antibody; chimera; light; heavy; chain; constant; variable; antigen; diagnosis; cancer; tumour.
XX	
OS	Mus musculus.
XX	
PN	WO902569-A.
XX	
PD	22-MAR-1990.
XX	
PP	08-SEP-1988; 88US-00241744.
XX	
PR	08-SEP-1988; 88US-00241744.
PR	13-SEP-1988; 88US-00243739.
PR	04-OCT-1988; 88US-00253002.
PR	19-JUN-1989; 89US-00387641.
PR	21-JUL-1989; 89US-0038276B.
XX	
PA	(ITGB-) INT GENETIC ENG INC.
PA	(INGE-) INGENE INT GENETIC.
XX	
PI	Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX	
DR	WPI; 1990-115825/15.
XX	
DR	N-PSDB; AAQ08604.
XX	
PT	Chimeric mouse-human antibodies - prep. using genes coding for constant human region murine variable region, esp. to 3 tumour antigen.
XX	
PS	Claim 13; Page 123 + Fig 14; 113pp; English.
XX	
CC	The sequence is used in the prodn. of a chimeric antibody mol. comprising two light chains and two heavy chains, each having a constant region (human) and a variable region (murine) having specificity to an antigen bound by murine monoclonal antibody (Mab) Br-3. The chimeric antibodies can be used for any purpose for which the original murine Mabs can be used, with the advantage that they are more compatible with the human body. They are esp. used for the diagnosis and treatment of cancer.
CC	(Updated on 25-MAR-2003 to correct PA field.)
XX	Sequence 131 AA;
PS	Query Match 95.4%; Score 555; DB 2; Length 131; Best Local Similarity 96.4%; Pred. No. 3.2e-39; 4; Indels 0; Gaps 0; Matches 106; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy	1 QAVVTOESALTTSPGTVTLCRCSRSTGAVTTSNSANWQEKPDHLFTGLIGGTINRVPGV
Db	20 QAVVTOESALTTSPGTVTLCRCSRSTGAVTTSNSANWQEKPDHLFTGLIGGTINRVPGV 99

Db	80 PARFSGSLIGDKAALITGTQTEDEATYFCALWYSNHWFGGGTKLIVLG 129	RESULT 6
ID	AAW06211	AAW06211 standard; protein; 131 AA.
XX		
AC	AAW06211;	
XX		
DT	25-MAR-2003 (revised)	
DT	12-FEB-1997 (first entry)	
XX	MAB Br-3 light chain variable region.	
KW	Chimeric antibody; monoclonal antibody; Br-3; antibody engineering; tumour; antigen; breast carcinoma; lung carcinoma; colon carcinoma; ovary carcinoma; cancer; diagnosis; therapy; light chain.	
KW	Mus sp.	
OS	XX	
XX	US5576184-A.	
PN		
PD	19-NOV-1996.	
XX		
PF	27-DEC-1994; 94US-00364001.	
XX		
PR	06-SEP-1988; 88US-00240524.	
PR	08-SEP-1988; 88US-00241744.	
PR	13-SEP-1988; 88US-00243739.	
PR	04-OCT-1988; 88US-00253002.	
PR	19-JUN-1989; 89US-00367641.	
PR	21-JUN-1989; 89US-00367641.	
PR	05-SEP-1989; 89WO-US003852.	
PR	06-MAY-1991; 91US-0065401.	
PR	06-MAY-1991; 91US-0065401.	
XX	(XOMA) XOMA CORP.	
PA		
XX	Chang CP, Lei S, Better MD, Robinson RR, Horwitz AH;	
XX	WPI; 1997-011249/01.	
DR	N-PSDB; AAT43436.	
XX		
PT	Chimeric mouse-human antibodies - recognise a human tumour antigen, used for the treatment and diagnosis of human cancers.	
PT	Example 3; Fig 14; 102pp; English.	
XX		
PS		
XX	The light chain variable region (AAW06211) of mouse monoclonal antibody Br-3 is the product of a cDNA clone (ATCC3436) isolated from a Br-3 hybridoma cDNA library. Mab Br-3 (IgG1) binds to an antigen that is expressed on the surface of human lung, breast, colon and ovary carcinomas, but not on most normal adult tissues. The light chain and heavy chain variable regions (see also AAW06212) of B38-1 can be linked to human constant regions and expressed in transformed host cells. Novel mouse-human chimeric antibodies (see also AAW06210 and AAW06213-18) can be produced that have specificity to human tumour antigens and can be used for the treatment and diagnosis of human cancer. (Updated on 25-MAR-2003 to correct PR field.)	
XX	Sequence 131 AA;	
SQ	Query Match 96.4%; Score 555, DB 2, Length 131; Best Local Similarity 96.4%; Pred. No. 3, 2e-39; Matches 106; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
Qy	1 QAVVTOESALTTSGETVTLCSSSTGAVTTSNSANWQEKDHLFTGLIGCTINRPGV 60	RESULT 7
Db	20 QAVVTOESALTTSGETVTLCSSSTGAVTTSNSANWQEKDHLFTGLIGCTINRPGV 79	AAW85058
Qy	61 PARFSGSLIGDKAALITGTQTEDEATYFCALWYSNHWFGGGTKLIVLG 110	AAW85058 standard; protein; 131 AA.
Db	80 PARFSGSLIGDKAALITGTQTEDEATYFCALWYSNHWFGGGTKLIVLG 129	AAW85058;
Db		20-MAR-2003 (revised)
Db		16-APR-1999 (first entry)
XX	Mouse Br-3 heavy chain variable region.	
XX	Heavy chain variable region; murine antibody Br-3; antibody ING-1; chimeric immunoglobulin; human tumour antigen; chimeric antibody; treatment; human cancer.	
KW	Mus sp.	
OS	XX	
PN	US5843685-A.	
PD	01-DEC-1998.	
XX		
PF	06-JUN-1995; 95US-00466034.	
XX		
PR	06-SEP-1988; 88US-00240624.	
PR	05-SEP-1988; 88US-00241744.	
PR	13-SEP-1988; 88US-00243739.	
PR	04-OCT-1988; 88US-00253002.	
PR	19-JUN-1989; 89US-00367641.	
PR	21-JUN-1989; 89US-0038768.	
PR	05-SEP-1989; 89WO-US003852.	
PR	06-MAY-1991; 91US-0065401.	
PR	27-DEC-1994; 94US-00364001.	
XX	(XOMA) XOMA CORP.	
PA		
XX	PI Horwitz AH, Lei S, Chang CP, Better MD, Robinson RR;	
XX	WPI; 1999-044574/04.	
DR	N-PSDB; AAT71154.	
XX		
PT	Chimeric antibody specific for human tumour antigen - useful as immunassay, imaging or anticancer agent.	
PT	Example 3; Fig 14; 92pp; English.	
XX		
CC	The present sequence represents the heavy chain variable region of murine antibody Br-3. The sequence was used to create chimeric mouse-human immunoglobulins which recognise the human tumour antigen bound by antibody ING-1 (produced by Hybridoma cell line ATCC HB 9812). The chimeric antibodies also have an antigen-binding site that competitively inhibits the binding of antibody ING-1, and mediate complement-dependent cytotoxicity of target cells or antibody-dependent cellular cytotoxicity to target cells. The chimeric antibodies can be used for therapeutic purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to correct PR field.)	
CC	Sequence 131 AA;	
SQ	Query Match 96.4%; Score 555, DB 2, Length 131; Best Local Similarity 96.4%; Pred. No. 3, 2e-39; Matches 106; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
Qy	1 QAVVTOESALTTSGETVTLCSSSTGAVTTSNSANWQEKDHLFTGLIGCTINRPGV 60	RESULT 8
Db	20 QAVVTOESALTTSGETVTLCSSSTGAVTTSNSANWQEKDHLFTGLIGCTINRPGV 79	AAW85058

Page
5

ID	AAR95949	standard; protein;	128 AA.
XX			
AC			
XX			
DT	11-FEB-1997	(first entry)	
XX			
DB	3G3 variable lambda chain.		
XX			
KW	Antibody; HNK-20; variable heavy chain; hybridoma; murine; IGA; mouse; F glycoprotein; respiratory syncytial virus; RSV; constant region gene; chimeric antibody; isotype-switched antibody; therapy; infection; human; pneumonia; bronchiolitis; animal.		
XX	Mus musculus.		
OS			
XX			
PD	06-JUN-1996.		
XX			
PR	01-DEC-1995;	95WO-US015716.	
XX			
PR	01-DEC-1994;	94US-00348548.	
XX			
PA	(ORAV-) ORAVAX INC.		
XX			
PT	DNA encoding variable region of antibody HNK-20 - for treating respiratory syncytial virus infection.		
XX			
PS	Example; Page 29; 75pp; English.		
XX			
CC	This sequence represents the variable lambda chain of an antibody produced by the 3G3 hybridoma cell line. AAR95949-R95948 represent sequences for variable regions of an antibody produced by the hybridoma cell line HNK-20. HNK-20 and 3G3 are murine hybridoma cell lines, that produces IgA specific for the F glycoprotein of respiratory syncytial virus (RSV). The DNA encoding these sequences were isolated using primers specific for the 5' untranslated region of the variable region, and for the intron downstream of the rearranged J region (see AAR30459-T30545 for primer sequences). The DNA encoding these sequences can be inserted into vectors containing heterologous (such as human) constant region genes, for the production of chimeric and isotype-switched antibodies. The antibodies are useful in the treatment and diagnosis of infection by RSV, such as pneumonia and bronchiolitis, in humans and animals. By using genomic DNA as a template, variable region genes can be isolated without producing fragments that have to be adapted for recombinant antibody expression. Also, by using the genomic DNA, no knowledge of the DNA sequence encoding the target variable region is required. Chimeric antibodies produced from these proteins, that contain the constant region of the host being treated, are less likely to cause adverse immune reactions.		
XX	Sequence 128 AA;		
SQ	Query Match 96.0%; Score 553; DB 2; Length 128; Best Local Similarity 97.2%; Pred. No. 4.e-39; Mismatches 105; Conservative 0; MisMatches 3; Indels 0; Gaps 0;	3 VVTOQSALTTSPGTWTCTRSSTGAVTTSNSANWYQEKPHLFGLGIGTINRPGV 60	3 VVTOQSALTTSPGTWTCTRSSTGAVTTSNSANWYQEKPHLFGLGIGTINRPGV 62
Qy	1 QAVVTOQSALTTSPGTWTCTRSSTGAVTTSNSANWYQEKPHLFGLGIGTINRPGV 60	20 QAVVTOQSALTTSPGTWTCTRSSTGAVTTSNSANWYQEKPHLFGLGIGTINRPGV 79	63 RFSSGLIGDKAALITTGAGTEDEAIYFCAWVSNHWVFGGGTKLTVIG 110
Db	61 PARFSGSLIGDKAALITTGAGTEDEAIYFCAWVSNHWVFGGGTKLTVIG 109	80 PARFSGSLIGDKAALITTGAGTEDEAIYFCAWVSNHWVFGGGTKLTVIG 128	RESULT 12
Qy	RESULT 12	PAR44990	ID AAY44990 standard; protein; 261 AA.
Db		AAV44990;	AC AAY44990;
XX			
DT	23-MAY-2000 (first entry)		
XX			
DB	Murine anti-Lewis Y antibody single-chain Fv fragment.		
RESULT 11			
AY03868			

XX
 KW Murine; Lewis Y; IgE; antibody; single-chain Fv fragment; scFv;
 heteromimbody; multifunctional compound; CH1-domain; CL-domain;
 heavy chain; constant domain; light chain; CD80 molecule; immunoglobulin;
 KW cytostatic; immunosupulatory; antileukaemia; diagnosis;
 anti-proliferative; prevention; treatment; malignant; haematopoietic cell;
 KW lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
 OS Mus sp.
 XX
 PH Location/Qualifiers
 FT Region 20 . 128
 /label= Immunoglobulin_light_chain_variable_region
 FT Region 144 . 261
 /label= Immunoglobulin_heavy_chain_variable_region
 XX
 PN WO20000605-A2.
 XX
 PD 10-FEB-2000.
 XX
 PP 28-JUL-1999; 99WO-EP005416.
 XX
 PR 28-JUL-1998; 98EP-00114082.
 XX
 PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
 XX
 PI Kufer P, Dreier T, Bauerle PA, Borschert K, Zettl R;
 XX
 DR WPI; 2000-195265/17.
 XX
 DR N-PDB; AZ25083.
 XX
 PT New multifunctional compounds useful for preventing and/or treating
 PT malignant cell growth and for detection and diagnosis.
 XX
 PS Claim 8; Fig 6; 16pp; English.
 XX
 CC The patient discloses heteromimbody which are multifunctional compounds
 CC producable in a mammalian host cell as a secretory and fully functional
 CC heterodimer of two polypeptide chains, where one of the polypeptide
 CC chains comprises, a CH1-domain (constant domain of an immunoglobulin
 CC heavy chain) and the other chain comprises CH1-domain (constant domain of
 CC an immunoglobulin light chain). The polypeptide chains further comprise,
 CC fused to the constant domains at least two (poly)peptides having
 CC different receptor or ligand functions, where further at least two of the
 CC different (poly)peptides lack an intrinsic affinity for one another and
 CC are linked via the constant domains. The heteromimbody have
 CC cytostatic, immunomodulatory, antileukaemia and anti-proliferative
 CC activities. These compounds can be used for diagnosing, preventing and
 CC treating malignant cell growth related to malignancies of haematopoietic
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
 CC melanomas and sarcomas. The present sequence is a murine anti-lewis Y
 CC antibody single-chain Fv (scFv) fragment which is used in the
 CC construction of heteromimbody comprising CH1 (first constant domain of
 CC human IgG1 heavy chain), CK (constant region of human Ig-kappa light
 CC chain) and CD80 molecule
 XX
 Sequence 261 AA;

XX
 ID ADM07542 standard; protein; 229 AA.
 XX
 AC ADM07542;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Murine immunoglobulin 15A2/2VIR light chain variable domain protein.
 XX
 KW murine; mouse; heavy; immunoglobulin;
 KW antibody; light chain variable domain; antiallergic; allergy; IgE;
 KW gene therapy; 15A2/2VIR.
 OS Mus sp.
 XX
 PN WO2003060080-A2.
 XX
 PD 24-JUL-2003.
 XX
 PP 20-DEC-2002; 2002WO-US041362.
 XX
 PR 21-DEC-2001; 2001US-0344874P.
 XX
 PA (IDEX-) IDEXX LAB INC.
 XX
 PI Krah ER, Guo H, Aiyappa A, Lawton R;
 XX
 DR WPI; 2003-598521/56.
 XX
 PT New canine heavy and light chain variable domain polypeptides, useful for
 PT treating canine allergy.
 XX
 PS Example 6; Fig 5; 130pp; English.
 XX
 CC The invention relates to a novel canine heavy or light chain variable
 CC domain polypeptide. The protein of the invention demonstrates
 CC antiallergic activity and may be useful for treating Canine allergy,
 CC possibly via gene therapy. The current sequence is that of a murine
 CC immunoglobulin light chain variable domain protein of the invention.
 XX
 SQ Sequence 229 AA;

Query Match	95.0%	Score	547	DB	7	Length	229
Best Local Similarity	96.3%	Pred.	No.	2.7e-38			
Matches	105	Conservative	0	Mismatches	4	Indels	0
Gaps	0						

QY 1 QAVVTOQSALTTSPGETWLTCTRSSTGAVTTSNSANWQEKPDHLPTGLIGGTINRVPGV 60
 Db 1 QAVVTOQSALTTSPGETWLTCTRSSTGAVTTSNSANWQEKPDHLPTGLIGGTINRVPGV 60
 QY 61 PARFSSGLGDKAALTTGAQTEDBAIYCALWYSNHWVGEGGKLTVL 109
 Db 61 PARFSSGLGDKAALTTGAQTEDBAIYCALWYSNHWVGEGGKLTVL 109

RESULT 14
 ID ADM07544
 XX
 AC ADM07544 standard; protein; 229 AA.
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Murine immunoglobulin 15A2/2VIR light chain variable domain protein.
 XX
 KW murine; mouse; heavy; immunoglobulin;
 KW antibody; light chain variable domain; antiallergic; allergy; IgE;
 KW gene therapy; 15A2/2VIR.
 OS Mus sp.
 XX
 PN WO2003060080-A2.
 XX
 PD 24-JUL-2003.

XX
XX 20-DEC-2002; 2002WO-US041362.
XX
XX PR 21-DEC-2001; 2001US-0344874P.
XX
PA (INDEX-) IDEXX LAB INC.
XX
PT Krah ER, Guo H, Aiyappa A, Lawton R;
XX DR WPI; 2003-598521/56.
XX
PT New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
PS Example 6; Fig 5; 130pp; English.

CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC anti-allergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a murine
CC immunoglobulin light chain variable domain protein of the invention.

SQ Sequence 230 AA:

Query Match 95.0%; Score 547; DB 7; Length 230;
Best Local Similarity 96.3%; Pred. No. 2.7e-38; Matches 105;
Mismatches 0; Conservative 0; Indels 0; Gaps 0;

QY 1 QAVVTOESALTTSPGRTVTTCRSSTGAVTTSANWVKRDPDHLFTGLIGGTINRVGV 60
Db 1 QAVVTOESALTTSPGRTVTTCRSSTGAVTTSANWVKRDPDHLFTGLIGGTINRVGV 60
QY 61 PARFSGSLIGDKKALTITGQTEDAEATYFCALWYSNHWVFGGGTKLTVL 109
Db 61 PARFSGSLIGDKKALTITGQTEDAEATYFCALWYSNHWVFGGGTKLTVL 109
Db 62 PARFSGSLIGDKKALTITGQTEDAEATYFCALWYSNHWVFGGGTKLTVL 110

Search completed: December 29, 2004, 17:57:32
Job time : 78.6047 secs

RESULT 15

ADM07543

ID ADM07543 standard; protein; 230 AA.

XX

AC ADM07543;

XX

DT 20-MAY-2004 (first entry)

XX

DE Murine immunoglobulin 15A2/1FBI light chain variable domain protein.

XX

KW murine; mouse; heavy; immunoglobulin;

KW antibody light chain variable domain; antiallergic; allergy; IgB;

XX gene therapy; 15A2/1FBI.

OS Mus sp.

XX

PN WO2003060080-A2.

XX

PD 24-JUL-2003.

XX

PP 20-DEC-2002; 2002WO-US041362.

XX

PR 21-DEC-2001; 2001US-0344874P..

XX

PA (INDEX-) IDEXX LAB INC.

XX

PT Krah ER, Guo H, Aiyappa A, Lawton R;

XX DR WPI; 2003-598521/56.

XX

New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.XX
PS Example 6; Fig 5; 130pp; English.

CC The invention relates to a novel canine heavy or light chain variable

OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	"[1]"
RP	SEQUENCE FROM N.A.: MEDLINE#82220143; PubMed=6283385;
RX	Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K., Baltimore D.; "Somatic variants of murine immunoglobulin lambda light chains."; Nature 298:380-382(1982).
RA	-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
RA	HSSP; P01724; IgV.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF0047; Ig_1.
DR	SMART; SM00406; IgV; 1.
DR	PROSITE; PS50835; Ig_LIKE; 1.
KW	Immunoglobulin V region; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 129 Ig lambda-1 chain V region S43.
FT	DOMAIN 20 125 Ig-like.
FT	NON_TER 129 129
SQ	SEQUENCE 129 AA; 13529 MW; 84E4E7DD5791345 CRC64;
RESULT 3	Query Match 95.8%; Score 552; DB 1; Length 129;
ID	Best Local Similarity 95.5%; Matches 105; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
LV1_B_MOUSE	STANDARD; PRT; 129 AA.
AC	P01724; 21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	01-OCT-2004 (Rel. 45, Last annotation update)
DE	Ig lambda-1 chain V regions MOPC 104E/RPC20/J558/S104 precursor.
OS	Mus musculus (Mouse)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10950; [1]
RN	SEQUENCE OF 1-29 (MOPC 104E), AND REVISIONS TO 20 AND 26. MEDLINE=77148916; PubMed=40522;
RA	Burstein Y., Schechter I.; "Amino acid sequence of the NH2-terminal extra piece segments of the precursors of mouse immunoglobulin lambda-type and kappa-type light chains."; Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
RT	SEQUENCE OF 20-129 (MOPC 104E AND RPC 20). MEDLINE=71107854; PubMed=5276767;
RA	Appella E.; "Amino acid sequences of two mouse immunoglobulin lambda chains."; Proc. Natl. Acad. Sci. U.S.A. 68:5190-5194(1971). [3]
RP	REVISIONS (MOPC 104E). MEDLINE=73229569; PubMed=4516208;
RA	Appella E.; Unpublished results, cited by:
RL	Cesari I.M., Weigert M.; Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973). [4]
RN	SEQUENCE OF 20-129 (J558 AND S104).
RESULT 4	Query Match 95.7%; Score 551; DB 1; Length 129;
ID	Best Local Similarity 95.5%; Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
O8VDE2	PRELIMINARY; PRT; 129 AA.
AC	O8VDE2; 01-MAR-2002 (TREMBLrel. 20, Created)
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)
RX	MEDLINE=73229569; PubMed=4516208;
RA	Cesari I.M., Weigert M.; "Mouse lambda-chain sequences."; Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973).
RT	No differences from MOPC 104E. The sequences of J558 and S104 seem identical with that shown.
RL	-!- MISCELLANEOUS: Compositions and partial sequences of RPC 20 show no differences from MOPC 104E. The sequences of J558 and S104 seem identical with that shown.
CC	-!- MISCELLANEOUS: These proteins were isolated from serum or urine of tumor-bearing mice.
CC	-!- MISCELLANEOUS: the MOPC 104E precursor was synthesized in a cell-free system directed by mRNA isolated from MOPC 1043 myeloma polyomes. Met-1 was lacking in 90% of the chains. It is probably rapidly cleaved after synthesis.
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	PIR; B93015; LIMS2B.
DR	PDB; 1AGU; X-ray; L=21-128.
DR	PDB; 1AGV; X-ray; L/M/N=20-129.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SM00406; IgV; 1.
DR	PROSITE; PS50835; Ig_LIKE; 1.
KW	3D-structure; Direct protein sequencing; Immunoglobulin V region; Pyrrolidone carboxylic acid; signal.
FT	SIGNAL 1 19
FT	CHAIN 20 129 Ig lambda-1 chain V regions MOPC 104E/RPC20/J558/S104.
FT	DOMAIN 20 125 Ig-like ² .
FT	MOD_RES 20 20
FT	STRAND 23 25
FT	TURN 31 31
FT	STRAND 33 34
FT	TURN 36 43
FT	STRAND 44 45
FT	TURN 45 46
FT	HELIIX 50 52
FT	STRAND 55 60
FT	TURN 61 63
FT	STRAND 64 70
FT	TURN 71 73
FT	STRAND 74 75
FT	TURN 77 78
FT	TURN 81 82
FT	STRAND 83 88
FT	TURN 89 90
FT	STRAND 91 97
FT	HELIIX 101 103
FT	STRAND 105 112
FT	STRAND 117 119
FT	STRAND 123 127
FT	NON_TER 129 129
SQ	SEQUENCE 129 AA; 13479 MW; 03629939D5791AC0 CRC64;

DT 01-OCT-2003 (REMBrel. 25, Last annotation update)
 DB Immunoglobulin Lambda chain variable region (Fragment).
 GN Name=4G12-A-H10;
 OS Mus musculus (mouse).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=spleen;
 RA Melle G.; Department of Ecole Supérieure de Technicien en
 RL Biologie Biochimie, Université Catholique de Lyon, Lyon, France.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=spleen;
 RA Blachere T.';
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ293694; CAC82790.1; --.
 DR HSSP; P0124; IAGV.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PSS0835; Ig_LIKE; 1.
 FT NON_TER 129 AA; 129 129 MW; C07F10303ADBB CRC64;
 SQ SEQUENCE 129 AA; 13565 MW; 010303ADBB CRC64;

Query Match 93.8%; Score 540; Pred. No. 2.2e-45; Length 129;
 Best Local Similarity 93.6%; Pred. No. 2.2e-45; Length 129;
 Matches 103; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QAVVTOESALTTSPGEVTWTCRSTGAVTNSANWQEKPDHLTFTGLIGGTINRPGV 60
 Db 20 QAVVTOESALTTSPGEVTWTCRSTGAVTNSANWQEKPDHLTFTGLIGGTINRPGV 79

Qy 61 PARFSSSLIGDKAALTITGAQTEDEAMVFCVLMWSNHWFEGGTKLTVLG 110
 Db 80 PARFSSSLIGDKAALTITGAQTEDEAMVFCVLMWSNHWFEGGTKLTVLG 129

RESULT 5

Q8CGS1 PRELIMINARY; PRT; 113 AA.

ID Q8CGS1; 01-MAR-2003 (REMBrel. 23, Created)
 DT 01-MAR-2003 (REMBrel. 23, Last sequence update)
 DR 01-MAR-2004 (REMBrel. 26, Last annotation update)
 DR Anti-deoxyribovalenol scfv lambda light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;
 RA Wang Z., Munshi K., Osawa F., Pestka J.J., Hart L.P.;
 DR Submitted (SERP) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY15141; AANT5453.1; --.
 DR HSSP; P0124; IAGV.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PSS0835; Ig_LIKE; 1.
 FT NON_TER 113 AA; 12034 MW; 0CAE4C65597E22BB CRC64;
 SQ SEQUENCE 113 AA; 12034 MW; 0CAE4C65597E22BB CRC64;

Query Match 93.0%; Score 535.5; Pred. No. 5.3e-45; Length 113;
 Best Local Similarity 94.6%; Pred. No. 5.3e-45; Length 113;

	Matches	105	Conservative	0	Mismatches	5	Indels	1	Gaps	1
Qy	1	QAVVTOESALTTSPGEVTWTCRSTGAVTNSANWQEKPDHLTFTGLIGGTINRPGV	60							
Db	1	QAVVTOESALTTSPGEVTWTCRSTGAVTNSANWQEKPDHLTFTGLIGGTINRPGV	60							
Qy	61	PARFSSSLIGDKAALTITGAQTEDEAMVFCVLMWSNHWFEGGTKLTVLG	110							
Db	61	PARFSSSLIGDKAALTITGAQTEDEAMVFCVLMWSNHWFEGGTKLTVLG	111							

RESULT 6

LVIC_MOUSE STANDARD; PRT; 110 AA.

ID LVIC_MOUSE STANDARD; PRT; 110 AA.

AC P01755; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DR 05-JUL-2004 (Rel. 44, Last annotation update)
 DB 19 Lambda 1 chain V region S178.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=73229669; PUBMED=4516208;
 RA Cesari I.M., Weigert M.;
 "Mouse Lambda-chain Sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973).
 CC -|- MISCELLANEOUS: This protein was isolated from serum or urine of tumor-bearing mice.
 CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSSP; P0124; IAGV.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PSS0835; Ig_LIKE; 1.
 DR KW Direct protein sequencing; Immunoglobulin V region.
 DR DOMAIN 1 106 Ig-like.
 FT NON_TER 110 AA; 110 MW; 7D06718EIA530205 CRC64;
 SQ SEQUENCE 110 AA; 11054 MW; 7D06718EIA530205 CRC64;

Query Match 92.7%; Score 534; DB 1; Length 110;
 Best Local Similarity 92.7%; Pred. No. 7.2e-45; Length 109;
 Matches 102; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QAVVTOESALTTSPGEVTWTCRSTGAVTNSANWQEKPDHLTFTGLIGGTINRPGV 60
 Db 1 QAVVTOESALTTSPGEVTWTCRSTGAVTNSANWQEKPDHLTFTGLIGGTINRPGV 60

Qy 61 PARFSSSLIGDKAALTITGAQTEDEAMVFCVLMWSNHWFEGGTKLTVLG 110
 Db 61 PARFSSSLIGDKAALTITGAQTEDEAMVFCVLMWSNHWFEGGTKLTVLG 110

RESULT 7

Q8ETI3 PRELIMINARY; PRT; 109 AA.

ID Q8ETI3; 01-MAR-2001 (REMBrel. 16, Created)
 AC Q8ETI3; 01-MAR-2001 (REMBrel. 16, Last sequence update)
 DR 01-MAR-2001 (REMBrel. 16, Last annotation update)
 DE Immunoglobulin light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;
 RA Song M.-Y, Kang H.-K., Kwag W.-J., Moon H.-J., Song T.-H., Ko I.-Y.,
 DR Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AR287275; ALG03053.1; -.

DR HSSP; P01724; IAGV.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; Ig_LIKE; 1.

FT NON_TER; 109; 1.

SQ SEQUENCE 109 AA; 11554 MW; 4F91E9D351B1E158 CRC64;

Query Match Best Local Similarity 93.6%; Pred. No. 1. 6e-44; DB 2; Length 109; Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 QAVVTOESALTTSPGETVTLLRSSTGAVTTSNSANWVQEKDHFLTGIGGTINRPGV 60

Db 1 QAVVTOESALTTSPGETVTLLRSSTGAVTTSNSANWVQEKDHFLTGIGGTINRPGV 60

RESULT 8

LV2B_MOUSE STANDARD; PRT; 129 AA.

ID _LV2B_MOUSE AC P01729; DT 21-JUN-1986 (Rel. 01, Last sequence update)

DT 21-JUL-1986 (Rel. 01, Last annotation update)

DR Ig_lambda-2 chain V region MOPC 315 precursor.

OS Mus musculus (Mouse).

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; [1]

RN RP SEQUENCE FROM N.A. MEDLINE=827421; PubMed=6287422;

RX Wu G.-B., Govindji N., Horumi N., Murialdo H.; RT "Nucleotide sequence of a chromosomal rearranged lambda 2 immunoglobulin gene of mouse."; RL Nucleic Acids Res. 10:3831-3843 (1982). RN RP SEQUENCE FROM N.A. MEDLINE=82220143; PubMed=6283385;

RX Bothwell A.L.M., Pakind M., Reth M., Imanishi-Kari T., Rajewsky K., RT "Somatic variants of murine immunoglobulin lambda light chains."; RL Nature 298:380-382 (1982). RN RP SEQUENCE OF 1-22. MEDLINE=9148758; PubMed=428562; RT Schechter I., Wolf O., Zemell R., Burstein Y.; RL "Structure and function of immunoglobulin genes and precursors."; Fed. Proc. 38:1839-1845 (1979). RN RP SEQUENCE OF 20-129. MEDLINE=74048693; PubMed=4760498; RX Dugan E.S., Bradshaw R.A., Simms E.S., Eisen H.N.; RT "Amino Acid sequence of the light chain of a mouse myeloma protein (MORC-315)." Biochemistry 12:5400-5416 (1973). RN [5] DETERMINATION OF AMIDATION STATES OF 58, 59, 62, 100, 102 AND 115. MEDLINE=8118754; PubMed=418802; RX Gavish M., Zakut R., Wilchek M., Givon D.; RT "Preparation of a semisynthetic antibody." Biochemistry 17:1445-1511 (1978). CC -1- MISCELLANEOUS: This chain is from a myeloma protein with anti-DNP activity. CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain. PIR: A93431; I2MS35. DR

DR HSSP; P01724; IAGV.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; Ig_LIKE; 1.

KW Direct Protein sequencing; Immunoglobulin v region; Pyrrolidone carboxylic acid; Signal.

FT SIGNAL 1 20 19 FT CHAIN 20 129 Ig lambda-2 chain v region; Pyrrolidone carboxylic acid.

FT DOMAIN 20 125 Ig-like.

FT MOD_RES 20 20 FT NON_TER 129 129

SQ SEQUENCE 129 AA; 13418 MW; 0AA6BB125723552C CRC64;

Query Match Best Local Similarity 88.2%; Pred. No. 8e-43; DB 1; Length 129; Matches 97; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 QAVVTOESALTTSPGETVTLLRSSTGAVTTSNSANWVQEKDHFLTGIGGTINRPGV 60

Db 2 QAVVTOESALTTSPGETVTLLRSSTGAVTTSNSANWVQEKDHFLTGIGGTINRPGV 79

Query Match Best Local Similarity 89.2%; Score 514; DB 1; Length 129; Matches 97; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 QAVVTOESALTTSPGETVTLLRSSTGAVTTSNSANWVQEKDHFLTGIGGTINRPGV 60

Db 2 QAVVTOESALTTSPGETVTLLRSSTGAVTTSNSANWVQEKDHFLTGIGGTINRPGV 110

RESULT 9

_LV2A_MOUSE STANDARD; PRT; 117 AA.

ID _LV2A_MOUSE AC P01723; DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DR 01-OCT-2004 (Rel. 45, Last annotation update)

DB Ig_lambda-1 chain V region precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; [1]

RN RP SEQUENCE FROM N.A. MEDLINE=79084170; PubMed=103630; RA Bernard O., Horumi N., Tonegawa S.; RT "Sequences of mouse immunoglobulin light chain genes before and after somatic changes"; RL Cell 15:1133-1144 (1978).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@ib-sib.ch).

CC -----

DR EMBL; V00811; CAA24193.1; -.

DR HSSP; P01724; IAGV.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003595; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; Ig_LIKE; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20 19 FT CHAIN 21 117 Ig lambda-1 chain v region.

FT DOMAIN 21 >117 Ig-like.

FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12222 MW; 36P3C5601C54B55A CRC64;

Query Match Best Local Similarity 84.5%; Score 487; DB 1; Length 117;

Best Local Similarity 96.9%; Pred. No. 3_3e-40; Matches 94; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 10

ID	LV2A_MOUSE	STANDARD;	PRT;	117 AA.
AC	P01728;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	IG lambda-2 chain V region precursor.			
OS	Mus musculus (Mouse)			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1] TAXID=10090;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=7017904; PubMed=418414;			
RA	Tongawa S., Maxam A.M., Tizard R., Bernard O., Gilbert W.;			
RT	"Sequence of a mouse germ-line gene for a variable region of an immunoglobulin light chain."			
RL	PROC. Natl. Acad. Sci. U.S.A. 75:1485-1489(1978).			
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
DR	EMBL; J00599; AAA39167.1; -;			
CC	EMBL; V00915; CAA24196.2; -;			
CC	EMBL; X58412; CAA41313.1; -;			
CC	EMBL; X58418; CAA41318.1; -;			
CC	EMBL; X58423; CAA41323.1; -;			
CC	EMBL; X58424; CAA41324.1; -;			
DR	PIR; A01996; L2NSWE.			
DR	HSSP; P01724; IgV.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IgV_1.			
DR	EMBL; J00599; AAA39167.1; -;			
DR	EMBL; V00915; CAA24196.2; -;			
DR	EMBL; X58412; CAA41313.1; -;			
DR	EMBL; X58418; CAA41318.1; -;			
DR	EMBL; X58423; CAA41323.1; -;			
DR	EMBL; X58424; CAA41324.1; -;			
DR	PIR; A01996; L2NSWE.			
DR	HSSP; P01724; IgV.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IgV_1.			
DR	PROSITE; PS50335; Ig_LIKE; 1.			
KW	immunoglobulin V region; Signal.			
FT	SIGNAL	1	20	
FT	CHAIN	21	117	Ig lambda chain V region 4A.
FT	DOMAIN	21	42	Framework-1.
FT	DOMAIN	43	55	Complementarity-determining-1.
FT	DOMAIN	56	71	Framework-2.
FT	DOMAIN	72	78	Complementarity-determining-2.
FT	DOMAIN	79	110	Framework-3.
FT	DOMAIN	111	117	Complementarity-determining-3.
FT	DISUFID	42	110	By similarity.
FT	NON_TER	117	117	
SEQ	SEQUENCE	117 AA;	12380 MW;	C507B0047CC1CD62 CRC64;
Query Match	48.4%; Score 279; DB 1; Length 117;			
Matches	60.6%; Pred. No. 1.1e-19;保守性 57; Mismatches 57; Conservative 9; Mismatches 9; Indels 0; Gaps 0;			
ID	LV0A_HUMAN	STANDARD;	PRT;	117 AA.
AC	P04211;			
DT	20-MAR-1987 (Rel. 04, Created)			
DT	20-MAR-1987 (Rel. 04, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG lambda chain V region 4A precursor.			
OS	Homo sapiens (Human)			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE.			
RT	Solomon A., Kyle R.A., Francione B.; "Light chain variable region subgroups of monoclonal immunoglobulins in amyloidosis AL";			

RL	(In) Gleanner G.G., Oserman E.F., Banditt B.P., Calkins E., Cohen A.S., Zucker-Franklin D. (eds); Amlylodosis, pp.449-462, Plenum Press, New York (1986).	Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RL	PIR; A01988; IGHST1.	DR EMBL; L43092; AAA69746.2; -.
DR	PDB; 1CD0; X-ray; A =1-111.	DR PIR; S7044; S7044.
DR	InterPro; IPR007110; Ig-like.	DR InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.	DR InterPro; IPR003596; Ig_v.
DR	InterPro; IPR003596; Ig_v.	DR InterPro; IPR003596; Ig_v.
DR	SMART; SM00406; Ig_v; 1.	DR SMART; SM00406; Ig_v; 1.
DR	PROSITE; PS50835; Ig_LIKE; 1.	DR PROSITE; PS50835; Ig_LIKE; 1.
KW	3D-structure; Direct protein sequencing; Immunoglobulin V region.	FT NON_TER 1 1
FT	DOMAIN 1 22	FT NON_TER 107 107
FT	DOMAIN 23 35	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	DOMAIN 36 50	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	DOMAIN 51 57	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	DOMAIN 58 91	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	DOMAIN 92 100	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	DISULFID 101 111	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	DISULFID 22 91	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	STRAND 4 5	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	STRAND 9 12	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	STRAND 14 15	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	STRAND 18 24	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	HELIX 29 31	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	STRAND 35 39	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	TURN 41 42	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	STRAND 46 50	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	TURN 51 53	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	STRAND 54 58	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	TURN 57 58	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	TURN 61 62	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	STRAND 63 68	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	TURN 69 72	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	STRAND 73 78	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	HELIX 83 85	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	STRAND 87 95	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	TURN 96 97	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	STRAND 98 102	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	STRAND 105 109	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
FT	NON_TER 111 111	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
SQ	NON_TER 111 AA; 12247 MW; 0941DD547D983598 CRC64;	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
RESULT 13	Query Match Score 424.5%; DB 1; Length 111; Best Local Similarity 46.4%; pred. No. 2-6e-16; Matches 51; Conservative 19; Mismatches 37; Indels 3; Gaps 2;	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
OY	3 VVTGGSLLTSPGETVLTNTRSSTGAUTNSANWQERPDHFLTGIGGTINRVPGPAR 61	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
Db	3 MLIOPHSVSVPSPGKIVIISCTRSRSGT1-AGCYYVWVQKQGRAPTVIFEDTORPSGVFD 61	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
OY	63 RFSGSL--1GDKAATITGQTEDAEIYFCALMWSNHMFGGGKLTLIG 110	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
Db	62 RFSGSIDRSSNSASLTISQTEDEADYCCSYDQRDHMWFGGGTKLTLIG 111	FT NON_TER 107 AA; 11306 MW; A2B04B37187A5P00 CRC64;
RA	RA Klaunser R.D., Collins F.S., Wagner L., Shearman C.M., Schuler G.D., Altshul S.R., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marsusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Scarce M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshimura S., Carninci P., Prange C., Raha S.S., Loquallano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madden A., Young A.C., Shevchenko Y., Bouffard G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Gilwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smialius D.B., Schnarch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN	RN [1] SEQUENCE FROM N.A.	RA EMBL; BC073795; AAH3795.1; -.
RC	RC TISSUE=Spleen;	DR InterPro; IPR003597; Ig-like.
RL	RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	DR InterPro; IPR007110; Ig-like.
DR	DR InterPro; IPR003597; Ig cl.	DR InterPro; IPR003597; Ig cl.
DR	DR InterPro; IPR003006; Ig_MHC.	DR InterPro; IPR003006; Ig_MHC.
DR	DR InterPro; IPR003596; Ig_v.	DR InterPro; IPR003596; Ig_v.
OC	OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	DR InterPro; IPR003599; Ig.
OX	OX NCBI_TaxID=9606;	DR InterPro; IPR007110; Ig-like.
RN	RN [1]	DR InterPro; IPR003597; Ig cl.
RP	RP SEQUENCE FROM N.A.	DR InterPro; IPR003006; Ig_MHC.
RC	RC Tissue=Spleen;	DR InterPro; IPR003596; Ig_v.
RA	RA Holmann A.;	DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IgC1; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig LIKE; 2.
 DR PROSITE; PS00290; Ig-MHC; UNKNOWN_1.
 KW Hypothetical protein.

SEQUENCE 236 AA; 24950 MW; 3B04772478478930 CRC64;

Query Match similarity 41.5%; Score 239; DB 2; Length 236;

Best Local similarity 46.0%; Pred. No. 2. 1e-15; Mismatches 37; Indels 4; Gaps 2; Matches 52; Conservative 20; MisMatches 37; Indels 4; Gaps 2;

QY 1 QAVVTQBSALTMSPGERTVLTCSRSTGAVTNSANSANVQEKEVDHLEFTGLGGTTINRPGV 60
 Db 20 OSVLQTQSSVSGTGPQRVITISCGSSNNI-GANNVWVQQLGTAPKULIHTNQRPSGV 78

QY 61 PARFSSSLIGKIAALTITGACTEDAEAYFCALW--YSNHWFGGETKLITIG 110
 Db 79 PPRPSCSKGPSASLVLISGLOSEDEABYYCAWDSDLDGPPVFGTGPKVTVLG 131

RESULT 15

LV2C_HUMAN

STANDARD; PRT; 111 AA.

ID LV2C_HUMAN . STANDARD; PRT; 111 AA.

AC P01706; .

DT 21-JUL-1985 (Rel. 01, Created)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ig Lambda chain V-II region BOH

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

REVDLINE=75115478; PubMed=804002;

RA Kohler H., Rudofsky S., Kuskeins L.;

RT "The primary structure of a human lambda II chain.";

J. Immunol. 114:415-421(1975).

-I- MISCELLANEOUS: This chain has the O2+ marker.

-I- MISCELLANEOUS: This chain was isolated from a myeloma protein.

-I- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR; A01972; LZTHBH.

HSSP; P01709; 2MCG.

DR Interpro; IPR003596; Ig_V.

DR SMART; PF00047; Ig; 1.

DR PROSITE; PS50835; Ig LIKE; 1.

DR PROSITE; PS50835; Ig LIKE; 1.

KW Direct protein sequencing;

KW Pyrrolidone carboxylic acid.

PT DOMAIN 1 106 Ig-like.

PT MOD_RBS 1 1 Pyrrolidone carboxylic acid.

PT DISURID 22 90 By similarity.

PT NON_TER 111 111

SQ SEQUENCE 111 AA; 11650 MW; 94503093262388 CRC64;

Query Match Similarity 41.1%; Score 236.5; DB 1; Length 111;

Best Local Similarity 44.1%; Pred. No. 1. 6e-15; Mismatches 49; Conservative 21; Mismatches 40; Indels 1; Gaps 1; Matches 49;

QY 1 QAVVTQBSALTMSPGERTVLTCSRSTGAVTNSANSANVQEKEVDHLEFTGLGGTTINRPGV 60

Db 1 OSALTOPRSVSGSPGSVTSICAGTSDDGGHNIFVSYOQHKGAKPLIIVGVNKRPSPGV 60

QY 61 PARFSSSLIGKIAALTITGACTEDAEAYFCALW--YSNHWFGGETKLITIG 110

Db 61 PYRFSSSKGNTASLTISGLOEDEAATYCCSYAGRFTWVGGTMLTVLG 111

Search completed: December 29, 2004, 18:05:20
 Job time : 77.9292 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

On protein - protein search, using sw model

Run on: December 29, 2004, 17:46:45 ; Search time 15.0885 Seconds

(without alignments) 701.451 Million cell updates/sec

Title: US-10-774-076-5
 Perfect score: 576
 Sequence: 1 QAVVTOQSAALTSPGSETVTL... ALWYSNHWVFGGGTKLTVLG 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqb, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

1 553 96.0 128 2 S22450

Ig lambda chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C;Accession: S52450

R;Berdoz, J.; Kraehnbaum, J.P.

submitted to the EMBL Data Library, November 1994

A;Description: Specific amplification by the polymerase chain reaction of rearranged ge

A;Reference number: S52445

A;Accession: S52450

A;Status: preliminary

A;Molecule type: DNA

A;Cross-references: EMBL:X82687; NID:673448; PIDN:CA58008.1; RID:673449

C;Genetics:

C;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>

C;Keywords: heterotrimer; immunoglobulin

F;34-111/Domain: immunoglobulin homology <IMM>

RESULT 1
 S52450
 Ig lambda chain V region - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 R;Berdoz, J.; Kraehnbaum, J.P.
 submitted to the EMBL Data Library, November 1994
 A;Description: Specific amplification by the polymerase chain reaction of rearranged ge
 A;Reference number: S52445
 A;Accession: S52450
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: EMBL:X82687; NID:673448; PIDN:CA58008.1; RID:673449
 C;Genetics:
 C;Introns: 16/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 F;34-111/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 553; DB 2; Length 128;

Best Local Similarity 97.2%; Pred. No. 1.5e-41; Mismatches 3; Indels 0; Gaps 0;

Matches 106; Conservative 0; MisMatches 3; Indels 0; Gaps 0;

Oy 1 QAVVTOQSAALTSPGSETVTL... ALWYSNHWVFGGGTKLTVL 109

Db 20 QAVVTOQSAALTSPGSETVTL... ALWYSNHWVFGGGTKLTVL 109

Oy 61 PARFSSGLIGDKAALITGAQTEDEAIYCALWYSNHWVFGGGTKLTVL 109

Db 80 PARFSSGLIGDKAALITGAQTEDEAIYCALWYSNHWVFGGGTKLTVL 109

RESULT 2
 PC4402
 DELB Leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein
 C;Species: synthetic

C;Accession: PC4402

C;Species: synthetic #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998

R;Suwai, C.; Ueda, H.; Suzuki, B.; Nagamune, T.

J; Biochem, 122, 322-329, 1997

A;Title: Construction, bacterial expression, and characterization of hapten-specific si

A;Reference number: PC4402

A;Accession: PC4402

A;Molecule type: DNA

A;Residues: 1-287 <SUZ>

C;Keywords: fusion protein

Query Match 96.0%; Score 553; DB 4; Length 287;

Best Local Similarity 97.2%; Pred. No. 3.4e-41; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

30	280.5	48.7	110	2	S57465	Ig lambda chain V-
31	279	48.4	117	1	I VHU2	Ig lambda chain pr
32	279	48.4	117	2	S04526	Ig lambda chain pr
33	277	48.1	98	2	S36062	Ig lambda chain -
34	250	43.4	98	2	S36063	Ig lambda chain -
35	247.5	43.0	108	2	S38498	Ig lambda chain V-
36	246.5	42.8	110	2	S57442	Ig lambda chain V-
37	244.5	42.4	111	1	I L6HUST	Ig lambda chain V-
38	244.5	42.4	216	2	A42193	Ig lambda chain (B
39	243.5	42.3	109	2	S19663	Ig lambda chain V
40	241	41.8	149	2	S23626	Ig lambda chain V
41	240	41.7	213	2	S21066	Ig lambda chain V
42	240	41.7	217	2	JR0246	Ig lambda chain NI
43	239.5	41.6	233	2	S25744	Ig lambda chain -
44	238.5	41.4	233	2	S25752	Ig lambda chain -
45	237.5	41.2	108	2	S47184	Ig lambda chain -

QY 1 QAVVTOESALTTSPGTTVLTCSRSTGAVTISANWQEKPDHLFTGLIGGTINRVPGV 60
Db 26 QAVVTOESALTTSPGTTVLTCSRSTGAVTISANWQEKPDHLFTGLIGGTINRVPGV 85
Qy 61 PARFSGSLIGDKAALTITGAOTEDBAIYFCALWYSNHWFGGSKTKLTVL 109
Db 86 PARFSGSLIGDKAALTITGAOTEDBAIYFCALWYSNHWFGGSKTKLTVL 134

RESULT 3
LMM4E
Ig lambda-1 chain precursor V regions (MOPC 104E, RPCC20, J558, S104, S178, H2020, S43)
C;Species: Mus musculus (house mouse)
C;Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004
C;Accession: B93815; B93775; C93775; A93784; B93784; C93784; A90780; G93282; A01995
R;Burstein, R.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74: 716-720, 1977
A;Title: Amino acid sequence of the NH₂-terminal extra piece segments of the precursors
A;Reference number: A93815; MUID:77148916; PMID:403522
A;Contents: MOPC 104E
A;Accession: B93815
A;Molecule type: protein
A;Residues: 1-29 <BUR>
A;Cross-references: UNIPROT:P01724
A;Note: this precursor was synthesized in a cell-free system directed by messenger RNA
d after synthesis
R;Appella, E.
Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971
A;Title: Amino acid sequences of two mouse immunoglobulin lambda chains.
A;Reference number: A93775; MUID:71107854; PMID:5276767
A;Contents: MOPC 104E; RPC 20
A;Accession: B93775
A;Molecule type: protein
A;Residues: Z', 21-25, 'Q', 27-129 <APP>
A;Accession: C93775
A;Molecule type: protein
A;Residues: 20-129 <APP>
A;Note: compositions and partial sequences of RPC 20 show no differences from MOPC 104E
R;Cesari, I.M.; Weigert, M.
Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973
A;Title: Mouse Lambda-chain sequences.
A;Reference number: A93794; MUID:73229669; PMID:4516208
A;Contents: J558; S104; S178
A;Accession: A93784
A;Molecule type: protein
A;Residues: 20-129 <CBS>
A;Accession: B93784
A;Molecule type: protein
A;Residues: 20-129 <CE2>
A;Accession: C93784
A;Molecule type: protein
A;Residues: 20-43, 'N', 45-70, 'N', 72-115, 'R', 117-129 <CH3>
A;Note: these proteins were isolated from serum or urine of tumor-bearing mice
R;Bernard, O.; Hozumi, N.; Tonegawa, S.
Cell 15, 1133-1144, 1973
A;Title: Sequences of mouse immunoglobulin light chain genes before and after somatic ch
A;Contents: A90780; MUID:79084170; PMID:103630
A;Accession: H2020
A;Molecule type: protein
A;Contents: S43
A;Accession: C93822
A;Molecule type: DNA
A;Residues: 1-58, 'B', 60-89, 'D', 91-98, 'T', 100-105, 'W', 107-129 <BOT>
A;Note: the sequence was determined from the differentiated gene
C;Comment: The MOPC 104E sequence is shown.

C;Genetics:
A;Intron: 16/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ-
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; pyroglutamic acid
R;1-19/Domain: Signal sequence #status experimental <SIG>
F;20-129/Domain: Ig lambda-1 chain precursor V region #status experimental <MAT>
F;34-111/Domain: immunoglobulin homology <IMM>
F;20/Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status experime
F;41-109/Disulfide bonds: #status predicted
Query Match 95.7%; Score 551; DB 1; Length 129;
Best Local Similarity 95.5%; Pred. No. 2, 3e-41;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
R;Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Gene 16, 237-239, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m
A;Reference number: PC4155; MUID:96194809; PMID:8647454
A;Accession: PC4156
A;Molecule type: mRNA
A;Residues: 1-214 <KNA>
A;Cross-references: GB:U8967; NID:gi1262178; PID:AC52488.1; PID:gi1262179
C;Species: Mus musculus (house mouse)
C;Accession: PC4156
F;1-214/Product: light chain #status predicted <MAT>
F;130-198/Domain: immunoglobulin homology <IMM>
Query Match 94.8%; Score 546; DB 2; Length 214;
Best Local Similarity 95.5%; Pred. No. 1e-01;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
R;Miller III, A.; Glaser, J.A.
J. Mol. Biol. 209, 763-778, 1990
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-m
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06818
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-112 <MLT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

RESULT 5
S06818
Ig lambda chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06818
Nature 298, 380-382, 1982
A;Title: Somatic variants of murine immunoglobulin lambda light chains.
A;Reference number: A93282; MUID:88220143; PMID:6283385
A;Contents: S43
A;Accession: C93822
A;Molecule type: DNA
A;Residues: 1-58, 'B', 60-89, 'D', 91-98, 'T', 100-105, 'W', 107-129 <BOT>
A;Note: the sequence was determined from the differentiated gene
C;Comment: The MOPC 104E sequence is shown.

F;15-92/Domain: immunoglobulin homology <IMM>

Query Match 93.0%; Score 535.5; DB 2; Length 112;
Best Local Similarity 94.5%; Pred. No. 4.4e-40; Mismatches 104; Conservative 2; Indels 3; Gaps 1;

Qy 2 AVTQESALITSPGETVLTCSRSTGAVTNSANWQEKPDHFLFTGLIGGTINRPGV 60
Db 1 AVTQESALITSPGETVLTCSRSTGAVTNSANWQEKPDHFLFTGLIGGTINRPGV 60

Qy 61 PARFSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVPGGTKL 106
Db 61 PARFSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVPGGTKL 106

RESULT 6
S06819
19 lambda chain V region (clone 10C3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C;Accession: S06819
R;Miller III, A.; Glazel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mouse
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06819
A;Molecule type: mRNA
A;Residues: 1-113 <ML>
A;Cross-references: EMBL:X17168; NID:952251; PIDN:CAA35046.1; PID:9930172
C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
C;Keywords: heterotetramer; immunoglobulin F14-91/Domain: immunoglobulin homology <IMM>
P;2-89/disulfide bonds: #status predicted

Query Match 92.4%; Score 532; DB 2; Length 113;

Best Local Similarity 95.4%; Pred. No. 9.1e-10; Mismatches 103; Conservative 1; Indels 0; Gaps 0;

Qy 2 AVTQESALITSPGETVLTCSRSTGAVTNSANWQEKPDHFLFTGLIGGTINRPGV 61
Db 1 AVTQESALITSPGETVLTCSRSTGAVTNSANWQEKPDHFLFTGLIGGTINRPGV 60

Qy 62 ARFGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVPGGTKL 109
Db 61 ARFGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVPGGTKL 108

RESULT 7
S02654
19 lambda chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S02654
R;Loman, M.; Faby, T.M.; Novick, K.E.; Monesier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Accession: S02639
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-106 <LOS>
A;Cross-references: EMBL:X65012; NID:952705; PIDN:CAA46145.1; PID:952706
C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
C;Keywords: heterotetramer; immunoglobulin F15-92/Domain: immunoglobulin homology <IMM>

Query Match 90.4%; Score 520.5; DB 2; Length 114;
Best Local Similarity 94.5%; Pred. No. 9.2e-39; Mismatches 103; Conservative 0; Indels 1; Gaps 1;

Qy 2 AVTQESALITSPGETVLTCSRSTGAVTNSANWQEKPDHFLFTGLIGGTINRPGV 60
Db 1 AVTQESALITSPGETVLTCSRSTGAVTNSANWQEKPDHFLFTGLIGGTINRPGV 60

Qy 61 PARFSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVPGGTKL 109
Db 61 PARFSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVPGGTKL 109

RESULT 8
B54256
Ig lambda 1 chain V region (hybridoma Se155-4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B54256; M4492
R;Bundle, D.R.; Eichler, R.; Gidney, M.A.; Meldal, M.; Ragauskas, A.; Sigurjóld, B.W.
Biochemistry 33, 5122-5132, 1994
A;Title: Molecular recognition of a *Salmonella* triaccharide epitope by monoclonal antibody
A;Reference number: A54256; MUID:94227048; PMID:751355
A;Accession: B54256
A;Molecule type: protein
A;Residues: 1-113 <RUN>
A;Experimental source: Se155-4 hybridoma, BALB/c mouse
A;Note: the sequence extracted from NCBI backbone (NCBIP:146746)
A;Note: the Se155-4 hybridoma is specific for the 3,6-dideoxy-D-galactose epitope of the antigen
C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
C;Keywords: heterotetramer; immunoglobulin F15-92/Domain: immunoglobulin homology <IMM>

Query Match 90.6%; Score 522; DB 2; Length 113;

Best Local Similarity 90.0%; Pred. No. 6.8e-39; Mismatches 99; Conservative 3; Indels 0; Gaps 0;

Qy 1 QAVTQESALITSPGETVLTCSRSTGAVTNSANWQEKPDHFLFTGLIGGTINRPGV 60
Db 1 QAVTQESALITSPGETVLTCSRSTGAVTNSANWQEKPDHFLFTGLIGGTINRPGV 60

Qy 61 PARFSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVPGGTKL 106
Db 61 PARFSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVPGGTKL 106

RESULT 10
L2MS35

Ig lambda-2 chain precursor V region (MOPC 315) - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: 31-Mar-98 #sequence_change 01-Dec-1995 #text_change 09-Jul-2004
 R;Wu, G.E.; Govindji, N.; Hozumi, N.; Murialdo, H.
 A;Title: Nucleotide sequence of a chromosomal rearranged lambda-2 immunoglobulin gene of
 A;Reference number: A93431; MUID:82274221; PMID:6287422
 A;Molecule type: mRNA
 A;Residues: 1-129 <WUG>
 A;Cross-references: UNIPROT:P01729
 R;Bothwell, A.L.M.; Paskind, M.; Reeth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.
 A;Note: the sequence was determined from the differentiated gene
 R;Schechter, I.; Wolf, O.; Zemel, R.; Burststein, Y.
 Fed. Proc. 38, 1839-1845, 1979
 A;Title: Structure and function of immunoglobulin genes and precursors.
 A;Reference number: A91462; MUID:7914878; PMID:28562
 A;Molecule type: DNA
 A;Accession: B91462
 A;Molecule type: protein
 A;Residues: 1-22 <SCIS>
 R;Dugan, E.S.; Bradshaw, R.A.; Simms, E.S.; Eisen, H.N.
 Biochemistry 12, 5400-5416, 1973
 A;Title: Amino acid sequence of the light chain of a mouse myeloma protein (MOPC-315).
 A;Reference number: A90372; MUID:74048693; PMID:4760498
 A;Molecule type: protein
 A;Residues: 20-24, 'E', '26-73, 'D', '75-129 <DUG>
 R;Gavish, M.; Zukut, R.; Wilchek, M.; Givol, D.
 Biochemistry 17, 1345-1351, 1978
 A;Title: Preparation of a semisynthetic antibody.
 A;Reference number: A90410; MUID:78187254; PMID:418802
 A;Molecule type: protein
 A;Residues: 1-129 <GAV>
 R;Bogen, B.; Lambrix, J.D.
 EMBO J. 8, 1947-1952, 1989
 A;Title: Minimum length of an idiotypic peptide and a model for its binding to a major T cell receptor.
 A;Reference number: S09391; MUID:50005397; PMID:2792076
 A;Molecule type: protein
 A;Residues: 1-10-126 <BOC>
 C;Comment: This chain is from a myeloma protein with anti-DNP activity.
 C;Complex: An immunogloulin heterotetramer subunit consists of two identical light (lambda) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; pyroglutamic acid
 F:1-19/Domain: signal sequence #status experimental <SIG>
 F:1-129/Domain: Ig lambda-2 chain precursor V region #status experimental <MAT>
 F:10-111/Domain: immunoglobulin homology <IMM>
 F:10-126/Region: idiotype to hisocompatibility complex class II #status experimental
 F:20/Modified site: Pyrrolidine carboxylic acid (Gln) (in mature form) #status experimental
 F:41-109/Disulfide bonds: #status predicted

Query Match 89.2%; Score 511; DB 1; Length 129;
 Best Local Similarity 88.2%; Pred. No. 3.9e-38; 7; Indels 0; Gaps 0;
 Matches 97; Conservative 6; Mismatch 7;

QY 1 QAVVTOESALITPSGETVTIICRSSTGAVTTSANWYQEKPHLFTGLIGGTRNRPGV 60
 Db 2 QAVVTOESALITPSGETVTIICRSSTGAVTTSANWYQEKPHLFTGLIGGTRNRPGV 79

QY 61 PARFGSLIGKQALKLTITGAQTEDEAYIFCALWVNHWRRGGTKLTIVLG 110
 Db 62 PARFGSLIGKQALKLTITGAQTEDEAYIFCALWVNHWRRGGTKLTIVLG 110

RESULT 11
 S06821
 Ig Lambda chain V region (clone 11C7) - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: S06821
 C;Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
 R;Miller III, A.; Glaser, J.A.
 J. Mol. Biol. 209, 763-778, 1989
 A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mouse Ig lambda chain V region antibodies
 A;Reference number: S06815; MUID:90064531; PMID:2555519
 A;Accession: S06821
 A;Molecule type: mRNA
 A;Residues: 1-113 <ML>
 A;Cross-references: EMBL:X17170; NID:95253; PID:CAA35048.1; PID:9930174
 A;Note: the authors translated the codon AGT for residue 47 as GLY, GTR for residue 56
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin F:14-91/Domain: Immunoglobulin homology <IMM>
 F:21-89/Disulfide bonds: #status predicted

Query Match 88.9%; Score 512; DB 2; Length 113;
 Best Local Similarity 90.8%; Pred. No. 5.1e-38; 1; Mismatches 9; Indels 0; Gaps 0;
 Matches 99; Conservative 9;

QY 2 AVVTOESALITPSGETVTIICRSSTGAVTTSANWYQEKPHLFTGLIGGTRNRPGV 61
 Db 1 AVVTOESALITPSGETVTIICRSSTGAVTTSANWYQEKPHLFTGLIGGTRNRPGV 60

QY 62 ARFGSGSLIGKQALKLTITGAQTEDEAYIFCALWVNHWRRGGTKLTIVLG 110
 Db 61 ARFGSGSLIGKQALKLTITGAQTEDEAYIFCALWVNHWRRGGTKLTIVLG 109

RESULT 12
 S05822
 Ig Lambda chain V region (clone 3B9) - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: S05822
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
 R;Miller III, A.; Glaser, J.A.
 J. Mol. Biol. 209, 763-778, 1989
 A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mouse Ig lambda chain V region
 A;Reference number: S06815; MUID:90064531; PMID:2555519
 A;Accession: S06822
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-114 <ML>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 C;Keywords: heterotetramer; immunoglobulin F:15-92/Domain: immunoglobulin homology <IMM>
 Query Match 88.8%; Score 511.5; DB 2; Length 114;
 Best Local Similarity 91.8%; Pred. No. 5.7e-38; 6; Indels 1; Gaps 1;
 Matches 101; Conservative 2; Mismatches 1;

QY 2 AVVTOESALITPSGETVTIICRSSTGAVTTSANWYQEKPHLFTGLIGGTRNRPGV 60
 Db 1 AVVTOESALITPSGETVTIICRSSTGAVTTSANWYQEKPHLFTGLIGGTRNRPGV 60

QY 61 PARFGSLIGKQALKLTITGAQTEDEAYIFCALWVNHWRRGGTKLTIVLG 110
 Db 62 PARFGSLIGKQALKLTITGAQTEDEAYIFCALWVNHWRRGGTKLTIVLG 110

RESULT 13
 S14582
 Ig Lambda chain V region - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Feb-1995 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
 C;Accession: S14582; S14587; S14588
 R;Chen, Q.; Stenzel-Poore, M.; Ritterberg, M.B.
 Submitted to the EMBL Data Library, March 1991
 A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH

A;Reference number: S14484
A;Accession: S14582
A;Molecule type: mRNA
A;Residues: 1-99 <CHE>
A;Cross-references: EMBL:X58654, NID:952911; PIDN:CAA41511.1; PID:952912
A;Experimental source: isolate PPC-1-54
A;Accession: S14587
A;Molecule type: mRNA
A;Residues: 1-99 <CH2>
A;Cross-references: EMBL:X58659, NID:952921; PIDN:CAA41516.1; PID:952922
A;Experimental source: isolate PPC-1-5
A;Accession: S14588
A;Molecule type: mRNA
A;Residues: 1-99 <CH3>
A;Cross-references: EMBL:X58660; NID:952923; PIDN:CAA41517.1; PID:952924
A;Experimental source: isolate PPC-15-30
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;15-92/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 498; DB 2; Length 99;
Best Local Similarity 96.0%; Pred. No. 7.4e-37; Indels 0; Gaps 0;
Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QAVVTOBSALTTSPGETVTILCRSSTGAVTNSANWQEKPDHIFTGLIGGTINRPGV 60
Db 1 OXVVIQTBOSALTTSPGETVTILCRSSTGAVTNSANWQEKPDHIFTGLIGGTINRPGV 60

Qy 61 PARFSSSLIGDKAALTITGAQTEDEAIYFCALWYSNHV 99
Db 61 PARFSSSLIGDKAALTITGAQTEDEAIYFCALWYSNHV 99

RESULT 14

PH1089
Ig lambda chain V region (clone 165-33) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C;Accession: PH1089
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J; Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell lines.

A;Reference number: PH0911; PMID:9238144; PMID:1512540

A;Accession: PH1089
A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA
A;Residues: 1-97 <TR1>

A;Experimental source: B cell, strain [NZB x NZW]F1

A;Cross-references: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin
P;15-92/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 487; DB 2; Length 97;

Best Local Similarity 96.9%; Pred. No. 6.6e-36; Indels 3; Gaps 0;

Matches 94; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QAVVTOBSALTTSPGETVTILCRSSTGAVTNSANWQEKPDHIFTGLIGGTINRPGV 60
Db 1 QAVVTOBSALTTSPGETVTILCRSSTGAVTNSANWQEKPDHIFTGLIGGTINRPGV 60

Qy 61 PARFSSSLIGDKAALTITGAQTEDEAIYFCALWYSNHV 97
Db 61 PARFSSSLIGDKAALTITGAQTEDEAIYFCALWYSNHV 97

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell lines.

A;Reference number: PH0971; PMID:9238144; PMID:1512540

A;Accession: PH1090
A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA
A;Residues: 1-97 <TR1>

A;Experimental source: B cell, strain [NZB x NZW]F1

A;Cross-references: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin
P;15-92/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 487; DB 2; Length 97;

Best Local Similarity 96.9%; Pred. No. 6.6e-36; Indels 3; Gaps 0;

Matches 94; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QAVVTOBSALTTSPGETVTILCRSSTGAVTNSANWQEKPDHIFTGLIGGTINRPGV 60
Db 1 QAVVTOBSALTTSPGETVTILCRSSTGAVTNSANWQEKPDHIFTGLIGGTINRPGV 60

Qy 61 PARFSSSLIGDKAALTITGAQTEDEAIYFCALWYSNHV 97
Db 61 PARFSSSLIGDKAALTITGAQTEDEAIYFCALWYSNHV 97

Search completed: December 29, 2004, 18:06:57
Job time : 16.2552 secs

RESULT 15

PH1090
Ig lambda chain V region (clone V-lambda-1) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C;Accession: PH1090
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J; Exp. Med. 176, 761-779, 1992

A;Residues: 1-99 <TR1>

A;Experimental source: B cell, strain [NZB x NZW]F1

A;Cross-references: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin
P;15-92/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 489.5; DB 2; Length 99;

Best Local Similarity 96.0%; Pred. No. 4.1e-36; Indels 1; Gaps 1;

Matches 96; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 QAVVTOBSALTTSPGETVTILCRSSTGAVTNSANWQEKPDHIFTGLIGGTINRPGV 60
Db 1 QAVVTOBSALTTSPGETVTILCRSSTGAVTNSANWQEKPDHIFTGLIGGTINRPGV 60

Qy 61 PARFSSSLIGDKAALTITGAQTEDEAIYFCALWYSNHV 100
Db 61 PARFSSSLIGDKAALTITGAQTEDEAIYFCALWYSNHV 99

THIS PAGE BLANK (USPSTF)

Copyright (c) 1993 - 2004 Compugen Ltd.

Om protein - protein search, using sw model

Run on: December 29, 2004, 18:05:34 ; Search time 63.5988 Seconds

622.182 Million cell updates/sec

Title: US-10-774-076-5

Perfect score: 576

Sequence: 1 QAVVTOESALTSRGETVTILCRSTGAVTTSNSANWQKPDHIFTGLIGGTINRPGV

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgm2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgm2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgm2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*

4: /cgm2_6/prodata/2/pubpaa/US05_PUBCOMB.pep:*

5: /cgm2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgm2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*

7: /cgm2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*

8: /cgm2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgm2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgm2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgm2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgm2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgm2_6/prodata/2/pubpaa/US10_PUBCOMB.pep:*

14: /cgm2_6/prodata/2/pubpaa/US10_PUBCOMB.pep:*

15: /cgm2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgm2_6/prodata/2/pubpaa/US10_PUBCOMB.pep:*

17: /cgm2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*

18: /cgm2_6/prodata/2/pubpaa/US11_NEW_PUB.pep:*

19: /cgm2_6/prodata/2/pubpaa/US60_NEW_PUB.pep:*

20: /cgm2_6/prodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	575	100.0	110	US-10-774-076-5
2	559	97.0	112	US-10-816-938-8
3	96.4	110	17	US-10-816-938-21
4	540	93.8	110	US-10-625-047-1
5	535	92.9	109	US-10-625-047-21
6	533	92.9	109	US-10-625-047-29
7	532	92.4	109	US-10-625-047-22
8	532	92.4	218	US-10-625-047-27
9	531	92.2	109	US-10-625-047-23
10	531	92.2	218	US-10-625-047-28
11	530	92.1	109	US-09-865-183-7
12	530.5	92.1	109	US-10-726-555-7
13	530	92.0	108	US-10-305-268-4

ALIGNMENTS

RESULT 1

Query Match Similarity 100.0%; Score 576; DB 17; Length 110;

Best Local Similarity 100.0%; Prod. No. 4e-46; Mismatches 0; Indels 0; Gaps 0;

Matches 110; Conservative 0; Mimatches 0; Index 0; Gaps 0;

Organism: mus sp.

SEQUENCE 1

QY 1 QAVVTOESALTSRGETVTILCRSTGAVTTSNSANWQKPDHIFTGLIGGTINRPGV

Db 1 QAVVTOESALTSRGETVTILCRSTGAVTTSNSANWQKPDHIFTGLIGGTINRPGV

SEQUENCE 2

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 3

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 4

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 5

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 6

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 7

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 8

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 9

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 10

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 11

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 12

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 13

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 14

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 15

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 16

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 17

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 18

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 19

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 20

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 21

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 22

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 23

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 24

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 25

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 26

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 27

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 28

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 29

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 30

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 31

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 32

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 33

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 34

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 35

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 36

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 37

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 38

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 39

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 40

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 41

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 42

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 43

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 44

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

SEQUENCE 45

QY 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

Db 61 PARPGSLIGDKAALITGCAQTEDEATCALWSNHNFGGGTKLTVLG

```

; Publication No. US20040229301A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Baiyang
; TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof
; FILE REFERENCE: 1861_1670002
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 8
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
; US-10-816-938-8

Query Match 97.0%; Score 559; DB 17; length 112;
Best Local Similarity 97.3%; Pred. No. 1.6e-44; 0; Mismatches 17; Conservative 0; Indels 0; Gaps 0;
Matches 107; Length: 112; Score: 559; DB: 17; SEQ ID NO: 8; PRIORITY: 1061-1570002; CURRENT FILING DATE: 2004-04-05; NUMBER OF SEQ ID NOS: 35; SOFTWARE: PatentIn version 3.2; SEQ ID NO: 21; LENGTH: 110
Db 61 PARFSGSLIGDKKALTTGAGTQDEAIYFCALWYSNHWVREGGTKTUVLG 110
Db 61 PARFSGSLIGDKKALTTGAGTQDEAIYFCALWYSNHWVREGGTKTUVLG 110

RESULT 3
US-10-816-938-21
; Sequence 21, Application US10816938
; Publication No. US20040229301A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Baiyang
; TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof
; FILE REFERENCE: 1861_1570002
; CURRENT FILING NUMBER: US10/816,938
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 21
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mus sp.
; US-10-816-938-21

Query Match 96.4%; Score 555; DB 17; length 110;
Best Local Similarity 96.4%; Pred. No. 3.6e-44; 1; Mismatches 106; Conservative 1; Indels 0; Gaps 0;
Matches 106; Length: 110; Score: 555; DB: 17; SEQ ID NO: 21; PRIORITY: 1061-1570002; CURRENT FILING NUMBER: US10/816,938; CURRENT FILING DATE: 2004-04-05; NUMBER OF SEQ ID NOS: 35; SOFTWARE: PatentIn version 3.2; SEQ ID NO: 21; LENGTH: 110
Db 1 QAVVTOESALTTSPGETVTILCRSSSTGAVTTSANWVQEKPHLFTCLIGGTINRPGV 60
Db 1 QAVVTOESALTTSPGETVTILCRSSSTGAVTTSANWVQEKPHLFTCLIGGTINRPGV 60
Qy 61 PARFSGSLIGDKKALTTGAGTQDEAIYFCALWYSNHWVREGGTKTUVLG 110
Db 61 PARFSGSLIGDKKALTTGAGTQDEAIYFCALWYSNHWVREGGTKTUVLG 110

RESULT 4
US-10-625-047-1
; Sequence 1, Application US106255047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Cornelle, Todd
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 23070-130910US
; CURRENT APPLICATION NUMBER: US/10/625,047
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 10/350,555
; PRIOR FILING DATE: 2003-01-23
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mus sp.
; US-10-625-047-1

Query Match 93.8%; Score 540; DB 17; length 110;
Best Local Similarity 93.6%; Pred. No. 3e-43; 1; Mismatches 103; Conservative 1; Indels 0; Gaps 0;
Matches 103; Length: 110; Score: 540; DB: 17; SEQ ID NO: 1; PRIORITY: 033070-130910US; CURRENT FILING NUMBER: US10/625,047; CURRENT FILING DATE: 2003-07-22; PRIOR APPLICATION NUMBER: US 10/350,555; PRIOR FILING DATE: 2003-01-23; SOFTWARE: PatentIn Ver. 2.1; SEQ ID NO: 21; LENGTH: 110
Db 1 QAVVTOESALTTSPGETVTILCRSSSTGAVTTSANWVQEKPHLFTCLIGGTINRPGV 60
Db 1 QAVVTOESALTTSPGETVTILCRSSSTGAVTTSANWVQEKPHLFTCLIGGTINRPGV 60
Qy 61 PARFSGSLIGDKKALTTGAGTQDEAIYFCALWYSNHWVREGGTKTUVLG 110
Db 61 PARFSGSLIGDKKALTTGAGTQDEAIYFCALWYSNHWVREGGTKTUVLG 110

RESULT 5
US-10-625-047-21
; Sequence 21, Application US10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Cornelle, Todd
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 033070-130910US
; CURRENT APPLICATION NUMBER: US10/625,047
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 10/350,555
; PRIOR FILING DATE: 2003-01-23
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURES:
; OTHER INFORMATION: native hybridoma murine 2D12.5 light chain
; US-10-625-047-21

Query Match 92.9%; Score 535; DB 17; length 109;
Best Local Similarity 93.6%; Pred. No. 2.6e-42; 1; Mismatches 102; Conservative 1; Indels 0; Gaps 0;
Matches 102; Length: 109; Score: 535; DB: 17; SEQ ID NO: 1; PRIORITY: 033070-130910US; CURRENT FILING NUMBER: US10/625,047; CURRENT FILING DATE: 2003-07-22; PRIOR APPLICATION NUMBER: US 10/350,555; PRIOR FILING DATE: 2003-01-23; SOFTWARE: PatentIn Ver. 2.1; SEQ ID NO: 21; LENGTH: 109
Db 1 AVVTOESALTTSPGETVTILCRSSSTGAVTTSANWVQEKPHLFTCLIGGTINRPGV 61
Db 1 AVVTOESALTTSPGETVTILCRSSSTGAVTTSANWVQEKPHLFTCLIGGTINRPGV 61
Qy 62 ARFSGSLIGDKKALTTGAGTQDEAIYFCALWYSNHWVREGGTKTUVLG 110
Db 61 ARFSGSLIGDKKALTTGAGTQDEAIYFCALWYSNHWVREGGTKTUVLG 110

```

CURRENT FILING DATE: 2003-07-22
 PRIORITY APPLICATION NUMBER: US 10/350,555
 PRIOR FILING DATE: 2003-01-23
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 29
 LENGTH: 109
 TYPE: PRT
 ORGANISM: Mus musculus
 FEATURE:
 OTHER INFORMATION: native hybridoma murine 2012.5 light chain
 US-10-625-047-29
 Query Match 92.9%; Score 535; DB 17; Length 109;
 Best Local Similarity 93.6%; Pred. No. 2.6e-42; Mismatches 1; Indels 0; Gaps 0;
 Matches 102; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 SEQ ID NO: 2
 1 AVVTOESALTTSPGETVTTCRSSTGAVTSNSANWQEKPDHIFTGLIGGTINRPGVP 61
 QY 62 ARFGSLIGKRALTTGQTEDEAIYFCALWISNHWFGGTKLTVL 110
 Db 61 ARFGSSLIGDKRALTTAGTQTEDEAIYFCALWISNHWFGGTKLTVL 109
RESULT 7
 US-10-625-047-22
 ; Sequence 22, Application US/10625047
 ; Publication No. US20040198962A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meares, Claude
 ; APPLICANT: Cornille, Todd
 ; TITLE OF INVENTION: Multi-functional Antibodies
 ; FILE REFERENCE: 023070-130910US
 ; CURRENT APPLICATION NUMBER: US10/625,047
 ; CURRENT FILING DATE: 2003-07-22
 ; PRIOR APPLICATION NUMBER: US 10/350,555
 ; PRIOR FILING DATE: 2003-01-23
 ; NUMBER OF SEQ ID NOS: 72 1
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 22
 ; LENGTH: 109
 ; TYPE: PRT
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:native cloned
 ; OTHER INFORMATION: Description of Artificial Sequence:mutant murine 2012.5 light chain variable
 ; OTHER INFORMATION: region (VL)
 ; US-10-625-047-22
 Query Match 92.4%; Score 532; DB 17; Length 109;
 Best Local Similarity 94.4%; Pred. No. 1e-41; Mismatches 0; Indels 0; Gaps 0;
 Matches 102; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 SEQ ID NO: 2
 1 AVVTOESALTTSPGETVTTCRSSTGAVTSNSANWQEKPDHIFTGLIGGTINRPGVP 61
 QY 62 ARFGSLIGDKRALTTGQTEDEAIYFCALWISNHWFGGTKLTVL 110
 Db 63 ARFGSSLIGDKRALTTAGTQTEDEAIYFCALWISNHWFGGTKLTVL 110
RESULT 8
 US-10-625-047-27
 ; Sequence 27, Application US/10625047
 ; Publication No. US20040198962A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meares, Claude
 ; APPLICANT: Cornille, Todd
 ; US-10-625-047-23
 Query Match 92.4%; Score 532; DB 17; Length 109;
 Best Local Similarity 94.4%; Pred. No. 1e-41; Mismatches 0; Indels 0; Gaps 0;
 Matches 102; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 SEQ ID NO: 23
 1 AVVTOESALTTSPGETVTTCRSSTGAVTSNSANWQEKPDHIFTGLIGGTINRPGVP 61
 QY 62 ARFGSLIGKRALTTGQTEDEAIYFCALWISNHWFGGTKLTVL 109
 Db 61 ARFGSSLIGDKRALTTAGTQTEDEAIYFCALWISNHWFGGTKLTVL 108
RESULT 9
 US-10-625-047-23
 ; Sequence 23, Application US/10625047
 ; Publication No. US20040198962A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meares, Claude
 ; APPLICANT: Cornille, Todd
 ; TITLE OF INVENTION: Multi-functional Antibodies
 ; FILE REFERENCE: 023070-130910US
 ; CURRENT APPLICATION NUMBER: US10/625,047
 ; CURRENT FILING DATE: 2003-07-22
 ; PRIOR APPLICATION NUMBER: US 10/350,555
 ; PRIOR FILING DATE: 2003-01-23
 ; NUMBER OF SEQ ID NOS: 72 1
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 23
 ; LENGTH: 109
 ; TYPE: PRT
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:native cloned
 ; OTHER INFORMATION: Description of Artificial Sequence:mutant murine 2012.5 light chain variable
 ; OTHER INFORMATION: region (VL)
 ; US-10-625-047-23
 Query Match 92.2%; Score 531; DB 17; Length 109;
 Best Local Similarity 94.4%; Pred. No. 6.3e-42; Mismatches 0; Indels 0; Gaps 0;
 Matches 102; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 SEQ ID NO: 2
 1 AVVTOESALTTSPGETVTTCRSSTGAVTSNSANWQEKPDHIFTGLIGGTINRPGVP 61
 QY 62 ARFGSLIGDKRALTTGQTEDEAIYFCALWISNHWFGGTKLTVL 109
 Db 61 ARFGSSLIGDKRALTTAGTQTEDEAIYFCALWISNHWFGGTKLTVL 108
RESULT 10
 QY 62 ARFGSLIGKRALTTGQTEDEAIYFCALWISNHWFGGTKLTVL 109
 Db 61 ARFGSSLIGDKRALTTAGTQTEDEAIYFCALWISNHWFGGTKLTVL 108

US-10-625-047-28
; Sequence 28, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; CORNEILLE, Todd
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 023070-130910US
; CURRENT APPLICATION NUMBER: US/10-625, 047
; CURRENT FILING DATE: 2003-07-22
; PRIORITY APPLICATION NUMBER: US 10/350, 555
; PRIORITY FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:N53C cloned
; OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable
; OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin
; OTHER INFORMATION: antibody kappa light chain constant region (VCL)
; US-10-625-047-28
Query Match 92.3%; Score 531; DB 17; Length 218;
Best Local Similarity 94.4%; Pred. No. 1.3e-41;
Matches 102; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 2 AVVTOQSALTTSPGERTVTLCRSSTGAUTSNANWQEKPDHFLPTGLIGCNRRPGVP 61
Db 3 AVVTOQSALTTSPGERTVTLCRSSTGAUTSNANWQEKPDHFLPTGLIGCNRRPGVP 62
Qy 62 ARFGSGSLIGDALITGQAQTEDAYFCAIYFCALWYSNHVWGGTKLIVL 109
Db 63 ARFGSGSLIGDALITGQAQTEDAYFCAIYFCALWYSNHVWGGTKLIVL 110
RESULT 11
US-03-865-483-7
; Sequence 7, Application US/09865483
; Patent No. US2002061581A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Jong Wook et al.
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOClonAL ANTIBODY AGAINST THE HBV S-SU
; TITLE OF INVENTION: ANTI-GENE AND A GENE ENCODING THE SAME
; FILE REFERENCE: 1599-0197P
; CURRENT APPLICATION NUMBER: US/03-29
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-865-483-7
Query Match 92.1%; Score 530.5; DB 9; length 109;
Best Local Similarity 93.6%; Pred. No. 6.9e-42;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
Qy 1 QAVVTOQSALTTSPGERTVTLCRSSTGAUTSNANWQEKPDHFLPTGLIGCTINRPGV 60
Db 1 QAVVTOQSALTTSPGERTVTLCRSSTGAUTSNANWQEKPDHFLPTGLIGCTINRPGV 60
Qy 61 PARFGSLIGDALITGQAQTEDAYFCAIYFCALWYSNHVWGGTKLIVL 110
Db 61 PARFGSLIGDALITGQAQTEDAYFCAIYFCALWYSNHVWGGTKLIVL 110
RESULT 12
US-10-726-555-7
; Sequence 7, Application US/10726555
; Publication No. US20040191259A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong Wook et al.
; TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
; FILE REFERENCE: 1599-0197P
; CURRENT APPLICATION NUMBER: US/10-726, 555
; CURRENT FILING DATE: 2003-12-04
; PRIORITY APPLICATION NUMBER: US/09/865, 483
; PRIORITY FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-10-726-555-7
Query Match 92.1%; Score 530.5; DB 17; Length 109;
Best Local Similarity 93.6%; Pred. No. 6.9e-42;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
Qy 1 QAVVTOQSALTTSPGERTVTLCRSSTGAUTSNANWQEKPDHFLPTGLIGCTINRPGV 60
Db 1 QAVVTOQSALTTSPGERTVTLCRSSTGAUTSNANWQEKPDHFLPTGLIGCTINRPGV 60
Qy 61 PARFGSLIGDALITGQAQTEDAYFCAIYFCALWYSNHVWGGTKLIVL 110
Db 61 PARFGSLIGDALITGQAQTEDAYFCAIYFCALWYSNHVWGGTKLIVL 110
RESULT 14
; Sequence 4, Application US/010305268
; Publication No. US2003012405A1
; GENERAL INFORMATION:
; APPLICANT: GRIFFITHS, GARY D.
; APPLICANT: GOVINDEAN, SERENGULAM V.
; APPLICANT: LOSMAN, MICHELLE
; APPLICANT: OU, ZHENXING
; TITLE OF INVENTION: ANTI-DOTA ANTIBODY
; FILE REFERENCE: 18733/1154
; CURRENT APPLICATION NUMBER: US/10/305, 268
; CURRENT FILING DATE: 2002-11-27
; PRIORITY APPLICATION NUMBER: 60/333, 479
; PRIORITY FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: IgIVL amino acid sequence
; US-10-305-268-4
Query Match 92.0%; Score 530; DB 14; Length 108;
Best Local Similarity 92.6%; Pred. No. 7.6e-42;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 3 VVTOQSALTTSPGERTVTLCRSSTGAUTSNANWQEKPDHFLPTGLIGCTINRPGV 62
Db 1 VVTOQSALTTSPGERTVTLCRSSTGAUTSNANWQEKPDHFLPTGLIGCTINRPGV 60
Qy 63 RPFGSLIGDALITGQAQTEDAYFCAIYFCALWYSNHVWGGTKLIVL 110
Db 61 RPFGSLIGDALITGQAQTEDAYFCAIYFCALWYSNHVWGGTKLIVL 109

US-10-328-190-14
; Sequence 14, Application US/10328190

; Publication No. US20030162709A1
; GENERAL INFORMATION:

; APPLICANT: ROSSI, EDMUND A.

; APPLICANT: GOLDENBERG, DAVID M.

; TITLE OF INVENTION: METHODS OF GENERATING MULTISPECIFIC, MULTIVALENT AGENTS

; FILE REFERENCE: 02418/015
; CURRENT APPLICATION NUMBER: US/10/328,190

; PRIORITY APPLICATION NUMBER: 60/3342,103
; PRIOR FILING DATE: 2001-12-26

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14

; LENGTH: 391
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Protein
; OTHER INFORMATION: Sequence for VL-chain of TSI
; US-10-328-190-14

Query Match 90.6%; Score 522; DB 14; Length 391;
Best Local Similarity 90.0%; Pred. No. 1..7e-40; Gaps 0;

Matches 99; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 QAVVTOESALUTSPGETVTUICRSSTGAVTNSANSANTVQSKPDHUTGLGGTINRPGV 60

Db 152 QTVVTOESALUTSPGETVTUICRSSTGAVTNSANWVQKRDHLPSGLIGGTNRAPGV 211

Qy 61 PARFSSLDIKAALTIGROTEDEAIYPCALWYSHHWVGGGTKLTVG 110

Db 212 PARFSSLDIKAALTIGQTEDBAYIFCYTWSDRWVQGGAKLTVG 261

RESULT 15

US-10-768-193-8

; Sequence 8, Application US/10768193
; Publication No. US20040181042A1

; GENERAL INFORMATION:

; APPLICANT: MEDICAL & BIOLOGICAL LABORATORIES CO., LTD.

; APPLICANT: The director of Chubu National Hospital

; APPLICANT: YANAGISAWA, Katsuhiro

; APPLICANT: SHIBATA, Masao

; TITLE OF INVENTION: Antibody recognizing GM1 ganglioside-bound

; TITLE OF INVENTION: amyloid b-protein and DNA encoding the antibody

; FILE REFERENCE: P0102402

; CURRENT APPLICATION NUMBER: US/10/768,193

; CURRENT FILING DATE: 2004-02-02

; PRIOR APPLICATION NUMBER: JP P2001-235700

; PRIOR FILING DATE: 2001-08-03

; PRIORITY APPLICATION NUMBER: PCT/JP02/07874
; PRIOR FILING DATE: 2002-08-01

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8

; LENGTH: 129
; TYPE: PRT

; ORGANISM: Mus musculus
; US-10-768-193-8

Query Match 90.1%; Score 519; DB 16; Length 129;
Best Local Similarity 90.0%; Pred. No. 9..7e-41; Gaps 0;

Matches 99; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QAVVTOESALUTSPGETVTUICRSSTGAVTNSANSANTVQSKPDHUTGLGGTINRPGV 60

Db 20 QAVVTOESALUTSPGETVTUICRSSTGAVTNSANWVQKRDHLPSGLIGGTNRAPGV 79

Qy 61 PARFSSLDIKAALTIGQTEDBAYIFCYTWSDRWVQGGAKLTVG 110

Db 80 PVFRSLSLIDKAALTITGAQTEDDAMYFCALWYSTHYVEGGTKVTVLG 129

Search completed: December 29, 2004, 18:42:00
Job time : 64.5988 secs

THIS PAGE BLANK (uspg)

GenCore version 5.1.6
copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 29, 2004, 17:38:43 ; Search time 80.0708 Seconds
(without alignments)
833.556 Million cell updates/sec

Title: US-10-774-076-4

Perfect score: 617.
Sequence: 1 EVOLOOGSGABELVRSQGVKL..... YGGTITTFAYNGQGTLTVVA 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02;*
1: uniprot_sprot;*
2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match Length	DB	ID	Description
1	489.5	79.3	468	2	Q99L31	
2	439.5	71.2	109	2	Q9JLB5	
3	413.5	67.0	473	2	Q9D8L2	
4	408.5	66.2	614	2	Q7TMF6	
5	407	66.0	139	2	Q924R5	
6	407	66.0	2	Q9PJB2		Mus musculus (Mouse).
7	407	66.0	465	2	AAH18280	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalii; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NCBI_TaxID=10090;
8	403.5	65.4	120	1	HV03_MOUSE	[1]
9	401	65.0	118	2	Q9ZI54	
10	401	65.0	139	1	HV07_MOUSE	
11	401	65.0	145	2	Q924Q7	
12	400.5	64.9	140	1	HV02_MOUSE	
13	400	64.8	136	2	Q7TPB3	
14	398	64.5	145	2	Q924R1	
15	397.5	64.4	146	2	Q924R8	
16	396	64.2	124	2	Q9UL92	
17	394	63.9	145	2	Q924Q6	
18	394	63.9	145	2	Q924R4	
19	394	63.9	473	2	Q99L25	
20	392.5	63.6	140	2	Q924R2	
21	392	63.6	142	2	Q924P1	
22	392	63.5	143	2	Q924P9	
23	391	63.4	143	2	Q91V67	
24	391	63.4	145	2	Q924R4	
25	390.5	63.3	142	2	Q924Q2	
26	390	63.2	141	2	Q924Q4	
27	390	63.2	145	2	Q924P3	
28	390	63.2	488	2	Q91WRI	
29	389.5	63.1	146	2	Q924Q3	
30	389	63.1	489	2	Q8VCK4	
31	389	63.0	2	Q924R0		

ALIGNMENTS

32	389	63.0	145	2	Q924P7	Q924P7 mub musculo
33	389	63.0	482	2	Q8K172	Q8K172 mub musculo
34	387.5	62.9	481	2	Q91WPI	Q91WPI mub musculo
35	387	62.7	137	2	Q924R6	Q924R6 mub musculo
36	386.5	62.6	146	2	Q924Q8	Q924Q8 mub musculo
37	385.5	62.5	472	2	Q924P5	Q924P5 mub musculo
38	385.5	62.5	144	2	AAH18535	AAH18535 mub musculo
39	384.5	62.3	454	2	AAH19337	AAH19337 homo sapi
40	384.5	62.3	143	2	Q924R7	Q924R7 mub musculo
41	384	62.2	463	2	Q99IC4	Q99IC4 mub musculo
42	384	62.2	480	2	Q6P899	Q6P899 homo sapi
43	383.5	62.2	480	2	AAH65733	AAH65733 homo sapi
44	383.5	62.1	613	2	Q8VCX7	Q8VCX7 mub musculo

DR	PROSIN; PS00290; IG_MHC; UNKNOWN_1.	DT	01-MAR-2004 (TREMBLrel. 26, last annotation update)
KW	Hypothetical protein.	DE	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone 181060009 product: immunoglobulin heavy chain 6 (heavy chain of IgM), full insert sequence.
SEQUENCE	468 AA; 51661 MW; 963523283332ADB CRC64;	DE	chain of IgM).
Best Local Similarity	79.3%; Score 489.5; DB 2; Length 468;	DR	Name=IgH-1a;
Matches	95; Conservative 10; Mismatches 19; Indels 7; Gaps 2;	GN	OS Mus musculus (Mouse).
Qy	1 EVLOQOSGAELVRSGASVKLCTASCPNPKYVHVKORPQHGLEWIGCDPNDTEY 60	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Db	20 EVQLQSQGAEVLVRPGASVKLCTASCPNIKOSIMHWVKORPQHGLEWIGCDPNDTEY 79	OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Qy	61 APNFORATMADTSNTAYQLSSTSEPAVYC---YGGITPAWQGQTLVTVS 115	NCBI_TaxID=10090;	[1]
Db	80 APKFQDQKATTDTSNTAYQLSSTSEPAVYCARNLNYGG--YYDYGQGTTIVS 137	RA	SEQUENCE FROM N.A.
Qy	116 A 116	RA	STRAIN=C57BL/6J; TISSUE=Pancreas;
Db	138 S 138	RA	NCBI_TaxID=920253; PubMed=10349636;
RESULT 2		RT	"High-efficiency full-length cDNA cloning.";
O9JL85	PRELIMINARY; PRT; 109 AA.	RL	Meth. Enzymol. 303:19-44(1999).
ID		RN	[2]
O9JL85		RP	SEQUENCE FROM N.A.
AC		RC	STRAIN=C57BL/6J;
O9JL85,	01-OCT-2000 (TREMBLrel. 15, last sequence update)	RA	MEIDLINE=2105660; PubMed=11217851;
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)	RT	"Functional annotation of a full-length mouse cDNA collection.";
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)	RL	Nature 409:485-560(2001).
DE	Anti-myosin immunoglobulin heavy chain variable region (Fragment)	RN	[3]
DE	Mus musculus (Mouse)	RP	SEQUENCE FROM N.A.
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	RC	STRAIN=C57BL/6J; TISSUE=Pancreas;
OC		RA	RIKEN FANOM Consortium;
OC		RA	The RIKEN Genome Exploration Research Group Phase I & II Team;
OX		RA	"Analysis of the mouse transcriptome based on functional annotation of Nature 420:563-573 (2002).
RN		RA	[4]
NCBI_TaxID=10090;		RP	SEQUENCE FROM N.A.
[1]		RC	STRAIN=C57BL/6J; TISSUE=Pancreas;
SEQUENCE FROM N.A.		RA	Medline=2049374; PubMed=1104159;
STRAIN=BALB/C;		RA	Carninci P., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RA		RT	Genome Res. 10:1617-1630(2000).
RA		RL	[5]
RA		RP	SEQUENCE FROM N.A.
RA		RC	STRAIN=C57BL/6J; TISSUE=Pancreas;
RA		RC	Medline=20530913; PubMed=11076861;
RA		RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akirama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura N., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Inegami T., Kashiwagi K., Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsubara S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequencing analysis (RISA) system-34-format sequencing pipeline with 384 multicapillary sequencer.";
RA		RT	Genome Res. 10:1757-1771(2000).
RA		RL	[6]
RA		RN	SEQUENCE FROM N.A.
RA		RC	STRAIN=C57BL/6J; TISSUE=Pancreas;
RA		RA	Adechi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirakata T., Horie F., Tomita K., Ishii Y., Itoh M., Izawa M., Kubisawa T., Kato H., Kawai J., Koima Y., Konno H., Kubo M., Koya S., Kurihara C., Matsuyama T., Mizraiki A., Nishi K., Nomura K., Numasaki K., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shitara Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamata T., Yasunishi A., Yoshida K., Yoshino M., Mikiyama M., Hayashizaki Y., "Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RA		DR	EMBL: AK007918; BAB25349.1; -.
RA		DR	PTR; PH165; PH165.
RA		DR	PTR; S19966; S19966.
RA		DR	PTR; S26746; S26746.
PRELIMINARY; PRT; 473 AA.			
09BL14;			
01-JUN-2001 (TREMBLrel. 17, Created)			
01-JUN-2001 (TREMBLrel. 17, Last sequence update)			

DR HSSP; P01864; 1B0G.
 DR MGD; MG1:96443; IgH-1a.
 DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
 DR GO; GO:0005771; C:multivesicular body; IDA.
 DR GO; GO:0003823; P:antigen binding; IDA.
 DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
 DR GO; GO:0030333; P:antigen processing; IDA.
 DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
 DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
 DR GO; GO:0008333; P:endosome to lysosome transport; IDA.
 DR GO; GO:0006911; P:phagocytosis; engulfment; IDA.
 DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
 DR GO; GO:0050871; P:positive regulation of B-cell activation; IDA.
 DR GO; GO:0050778; P:positive regulation of immune response; IDA.
 DR GO; GO:005766; P:positive regulation of phagocytosis; IDA.
 DR GO; GO:000112; P:positive regulation of type I hypersensitivity; IDA.
 DR GO; GO:0001798; P:positive regulation of proteolysis and peptidolysis; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig CL.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig V.
 DR Pfam; PF07654; C1-set; 4.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00405; IgV; 1.
 DR PROSITE; PS50335; IG LIKE; 4.
 DR PROSITE; PS50390; IG MHC; UNKNOWN 1.
 DR SEQUENCE; 473 AA; 51699 MW; 9DED57A514475FB CRC64;

Query Match, Best Local Similarity 67.0%; Score 413.5; DB 2; Length 473; Matches 81; Conservative 14; Mismatches 21; Indels 3; Gaps 1;

Qy 1 EVQLQSGAELVRSAGSVKLSTASGPNIKDYIHWVKORPQEGLWIGCIDPENGTEY 60
 Db 20 OVOLOQSGAELVRSAGSVKLSTASGPNIKDYIHWVKORPQEGLWIGCIDPENGTEY 79
 Qy 61 APNFGQRATMTADTSNTAYLQQLSITSENTAVYYCYGGTIT--FAYWQGQTLYTVSA 116
 Db 80 NEKFKGKATUTADKSSTSAYMQLSSLTSEDASAVIFCARSDYDWFAYWQGQTLYTVSA 138

RESULT 4

Q7TM6 PRELIMINARY; PRT; 614 AA.
 AC Q7TM6;
 DT 01-OCT-2003 (TREMBREL. 25, Created)
 DT 01-MAR-2004 (TREMBREL. 26, Last annotation update)
 DE MG60843 protein.

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [1]

RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic stem cell;

RX MEDLINE-2238257; Pubmed=1247793;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhattacharya R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueline N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarante P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Heaton B., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Tschimann J.W., Green R.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., RA

RA Krzywinski M.I., Salska U., Smalius D.B., Schenrich A., Schein J.B., Jones S.J., Marr M.A.; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell; Strausberg R.; Submitted (Jun-2003) to the EMBL/GenBank/DDBJ databases.

RL EMBL; BC053409; ARMS3405; 1; -.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig CL.

DR InterPro; IPR003006; Ig MHC.

DR InterPro; IPR003596; Ig V.

DR Pfam; PF07654; C1-set; 4.

DR SMART; SM00405; IgV; 1.

DR PROSITE; PS50335; IG LIKE; 5.

DR PROSITE; PS50290; IG MHC; UNKNOWN 3.

DR SEQUENCE; 614 AA; 67746 MW; 839BAFBBD124P89 CRC64;

Query Match, Best Local Similarity 66.2%; Score 408.5; DB 2; Length 614; Matches 78; Conservative 55; Mismatches 20; Indels 3; Gaps 1;

Qy 1 EVQLQSGAELVRSAGSVKLSTASGPNIKDYIHWVKORPQEGLWIGCIDPENGTEY 60
 Db 20 OVOLOQSGAELVRSAGSVKLSTASGPNIKDYIHWVKORPQEGLWIGCIDPENGTEY 79

RESULT 5

Q924R5 PRELIMINARY; PRT; 139 AA.

AC Q924R5;
 DT 01-DEC-2001 (TREMBREL. 19, Created)
 DT 01-DEC-2001 (TREMBREL. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBREL. 25, Last annotation update)

DE VH186.2-D-J-C mu protein (Fragment).

GN Name=VH186.2-D-J-C mu;

OC Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [1]

RN NCBI_TAXID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RA Kozono Y., Kozono H., Azuma T.; Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.

DR PIR; PH1137; PHM137.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00405; IgV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

FT NON_TER 139 139 139

FT SEQUENCE 139 AA; 15221 MW; 8491E2P85614736A CRC64;

Query Match, Best Local Similarity 66.0%; Score 407; DB 2; Length 139; Matches 78; Conservative 14; Mismatches 22; Indels 2; Gaps 1;

Qy 1 EVQLQSGAELVRSAGSVKLSTASGPNIKDYIHWVKORPQEGLWIGCIDPENGTEY 60
 Db 1 OVOLOQSGAELVRSAGSVKLSTASGPNIKDYIHWVKORPQEGLWIGCIDPENGTEY 60

61 APNFGQRATMTADTSNTAYLQQLSITSENTAVYYCYGGTITFAYWQGQTLYTVSA 116

OC Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10890;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=3131846; PubMed=6186498;
 RA Siekavitz M.; Gefter M.L.; Brodeur P.; Riblet R.
 RA Marshak-Rothstein A.;
 RT "The genetic basis of antibody production: the dominant anti-arsonate
 idiotype response of the strain A mouse.";
 RL Bur. J. Immunol. 12:1023-1032(1982).
 -I MISCELLANEOUS: From analysis of the sizes of several other
 differentiated genes that hybridize to this one, the authors
 conclude that all of these V regions have rearranged to the same J
 segment, JH2.

-I SIMILARITY: Contains 1 immunoglobulin-like domain.

PDB: 1JFQ; X-ray; H1-120.

DR InterPro: IPR007110; Ig-like.

DR Pfam: PF00047; Ig; 1.

SMART: SM00406; IgV; 1.

PROSITE: PS50315; Ig_LIKE; 1.

3D-STRUCTURE: Hybridoma; Immunoglobulin V region.

KW DOMAIN 1 111.

PT NON_TER 120 120

SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 65.4%; Score 403.5; DB 1; Length 120;

Best Local Similarity 64.2%; Pred. No. 2.9e-33;

Matches 77; Conservative 17; Mismatches 21; Indels 5; Gaps 1;

QY 2 VOLQSGAELVRSQAVKLSCTASAGNIKQYIHWKQRBQGLEWIGCIPDENDEYA 61

Db 1 VOLQSGAELVRSQAVKLSCTASAGNIKQYIHWKQRBQGLEWIGCIPDENDEYA 60

QY 62 PNFGOCRATMADTSNTAYQLQSLISLTSEDATAVYVYC----YGGTTFAYWQGQTLYVA 116

Db 61 BKFKGKTTLVDKSSSTAYMLRSLISEDSAVIFCARSVYGGSYFDYWGQGTIVSS 120

RESULT 9

Q9ZIC4 PRELIMINARY; PRT; 118 AA.

Q9ZIC4; 01-MAY-1999 (TREMBREL. 10, Last sequence update)

DT 01-OCT-2003 (TREMBREL. 25, Last annotation update)

DB Anti-porcine VCAM mab 3F4 heavy chain variable region (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;

OC Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

CC STRAIN=C7BL/6;

RX MEDLINE=8123448; PubMed=6798376;

RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,

RA Baltimore D.

RT "Heavy chain variable region contribution to the Npb family of

antibodies: somatic mutation evident in a gamma 2a variable region.";

RL Cell 24:625-637 (1981).

CC -I MISCELLANEOUS: The Bl-g mu chain mRNA was cloned from a hybridoma

making antibodies to the hapten (-hydroxy-3-nitrophenyl)acetyl

(Npb antibodies).

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to licensee@sb-sib.ch).

CC DR EMBL; J00529; AAA38170.1; -.

CC DR PIR; A90099; MMS18.

DR PDB; 1AGU; X-ray; H-20-139.

DR PDB; 1AGW; X-ray; H-20-139.

DR PDB; 1NQB; X-ray; A/C=20/139.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; Ig_LIKE; 1.

DR 3D-STRUCTURE: Immunoglobulin v region; Signal.

FT CHAIN 20 139

FT DOMAIN 20 49

FT DOMAIN 50 54

FT DOMAIN 55 68

FT DOMAIN 69 85

FT DOMAIN 86 117

FT DOMAIN 118 124

FT DOMAIN 125 139

FT DISOIFID 41 115

FT STRAND 22 24

FT STRAND 28 31

FT TURN 33 34

FT STRAND 37 44

FT HELIX 48 50

FT STRAND 52 58

Query Match 1 64.9%; Score 400; DB 1; Length 140;
 Best Local Similarity 63.6%; Pred. No. 7e-33; Mismatches 23; Indels 5; Gaps 1;

DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 145 145
 SQ SEQUENCE 145 AA; 16141 MW; 55A59A790BB2CD6A CRC64;
 Query Match 1 65.0%; Score 401; DB 2; Length 145;
 Best Local Similarity 63.3%; Pred. No. 6.5e-33; Mismatches 23; Indels 4; Gaps 1;
 Matches 76; Conservative 17; Mismatches 23; Indels 4; Gaps 1;

DR 1 61 APNFGQRTMTADTSNTAYLQLSLSSTSDAVYKC---YGGTTPAYWQGQTIVTVA 116
 DR 1 QVOLQPGELVRKGASVNLCKSGYTPSTWMWVHQKQRQGRGLWIGRIDPNSSGTKV 60
 DR 1 NEKFKSKATLTVDKPSSTAQMQLSLTSEDSAVIDYQSYFDYNGQQTIVTVA 139

Query Match 1 65.0%; Score 401; DB 1; Length 139;
 Best Local Similarity 63.3%; Pred. No. 6.5e-33; Mismatches 23; Indels 4; Gaps 1;
 Matches 76; Conservative 17; Mismatches 23; Indels 4; Gaps 1;

DR 1 61 APNFGQRTMTADTSNTAYLQLSLSSTSDAVYKC---YGGTTPAYWQGQTIVTVA 116
 DR 1 QVOLQPGELVRKGASVNLCKSGYTPSTWMWVHQKQRQGRGLWIGRIDPNSSGTKV 60

RESULT 11

OQ 1 EVOLOQSGAEVLVSGASVNLCKSGYTPSTWMWVHQKQRQGRGLWIGRIDPNSSGTKV 60
 DR 20 QVOLQPGELVRKGASVNLCKSGYTPSTWMWVHQKQRQGRGLWIGRIDPNSSGTKV 79

Query Match 1 61 APNFGQRTMTADTSNTAYLQLSLSSTSDAVYKC---YGGTTPAYWQGQTIVTVA 116
 DR 01-OCT-2001 (Tremblrel. 19, Last sequence update)
 DR 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DR VH186_2-D-J-C mu protein (Fragment).
 DR Name=VH186_2-D-J-C mu;
 DR Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 NCBI_TAXID=10050;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C5BL/6;
 RA Kozono Y., Kozono H., Azuma T.,
 RQ submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB007793; BAB83278.1; --.
 DR F28833; FB8833.
 DR PIR; PH1105; PH1105.
 DR PIR; PH1108; PH1108.
 DR PIR; PH1114; PH1114.
 DR PIR; PH1118; PH1118.
 DR PIR; PH1119; PH1119.
 DR PIR; PH1125; PH1125.
 DR PIR; PH1126; PH1126.
 DR PIR; PH1128; PH1128.
 DR PIR; PH1129; PH1129.
 DR PIR; PH1131; PH1131.
 DR PIR; PH1134; PH1134.
 DR PIR; PH1137; PH1137.
 DR PIR; PH1139; PH1139.
 DR PIR; PH1142; PH1142.
 DR PIR; PH1144; PH1144.
 DR PIR; PH1147; PH1147.
 DR PIR; PH1149; PH1149.
 DR PIR; PH1150; PH1150.
 DR PIR; PH1151; PH1151.
 DR PIR; PH1152; PH1152.
 DR PIR; PH1153; PH1153.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003586; Ig_V.

RESULT 12

HV02_MOUSE ID HV02_MOUSE STANDARD; PRT; 140 AA.
 DR P01745; 21-JUL-1986 (Rel. 01, Created)
 DR 21-JUL-1986 (Rel. 01, Last sequence update)
 DR 10-OCT-2003 (Rel. 42, Last annotation update)
 DR 19 heavy chain V region 93G7 precursor.

OS Mus musculus (Mouse);
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RA Capra J.D.;
 RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
 RA MEDLINE=82152818; PubMed=6801765;
 RA SIMS J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
 RA SEQUENCE FROM N.A.
 RC STRAIN=A/J;
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to licensee@isb-sib.ch).
 DR EMBL; J00493; AAA38128.1; --.
 DR PIR; AA94264; HMGSC7.
 DR HSSP; P0147; IJFQ.
 DR InterPro; IPR007110; Ig_Like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 KW Hydridoma; Immunoglobulin V region; signal.
 FT SIGNAL 1 19
 FT CHAIN 20 140 Ig heavy chain V region 93G7.
 FT DOMAIN 20 139 Ig-like.
 FT NON_TER 140 140
 SQ SEQUENCE 140 AA; 15514 MW; 25A4CB831DA5CE8 CRC64;

Query Match 1 64.9%; Score 400; DB 1; Length 140;
 Best Local Similarity 63.6%; Pred. No. 7e-33; Mismatches 23; Indels 5; Gaps 1;

DR 1 61 APNFGQRTMTADTSNTAYLQLSLSSTSDAVYKC---YGGTTPAYWQGQTIVTVA 116
 DR 20 QVOLQPGELVRKGASVNLCKSGYTPSTWMWVHQKQRQGRGLWIGRIDPNSSGTKV 60

Page 8

DR	PIR; PH1137;	PH1137.
DR	PIR; PH1139;	PH1139.
DR	PIR; PH1142;	PH1142.
DR	PIR; PH1144;	PH1144.
DR	PIR; PH1147;	PH1147.
DR	PIR; PH1149;	PH1149.
DR	PIR; PH1150;	PH1150.
DR	PIR; PH1151;	PH1151.
DR	PIR; PH1152;	PH1152.
DR	PIR; PH1153;	PH1153.
DR	INTERPRO; IPR07110;	IG-like.
DR	INTERPRO; IPR03596;	IG_v.
DR	PTam; PP0047;	IG; 1.
DR	SMART; SMD0406;	IGv; 1.
DR	PROSITE; PS50835;	IG-LIKE; 1.
NON_TER	1	1
FT	146	146
SEQUENCE	AA;	MW;
SQ	146 AA;	92460P1FDR1B7538 CRC64;

Query Match 64.4%; Score 397.5; DB 2; Length 146;
 Best Local Similarity 62.8%; Pred. No. 1.5e-32;
 Matches 76; Conservative 18; Mismatches 22; Indels 5; Gaps 2;

QY	Db	QY	Db
1 EVOLOQSACBLURSGASTYKSLCPASSGENIKDYIHHWVKORPREGLEWIGCIDIENGDTET	60	1 QVOLQOPCAELVKPGASTYKLSCKRASGYIPTSYWMHWVKQRPGRLIEWIGRIDPNGGTKY	60
61 AENFOGRATMADTSNAYLOSSLSEDATAVYC---YGMJ-TRAYWGQCLTVS	115	61 NEKPKSKATLTUVKPSSTAYMOLSSLSEDSATYYCARSYYGSSLYYFDYWGOGTUTVS	120

Search completed: December 29, 2004, 18:05:18
Job time : 80.0708 secs

Search completed: December 8, 2007

GenCore version 5.1.6									
Copyright (c) 1993 - 2004 Compugen Ltd.									
OM protein - protein search, using sw model									
Run on:	December 29, 2004, 17:46:45 ; Search time 15.9115 Seconds								
Title:	US-10-774-076-4								
Perfect score:	617								
Sequence:	BLOSUM62								
Scoring table:	Gappen 10.0 , Gapext 0.5								
Searched:	283416 seqs, 96216763 residues								
Total number of hits satisfying chosen parameters:	283416								
Minimum DB seq length: 0									
Maximum DB seq length: 200000000									
Post-processing: Minimum Match 0%									
Maximum Match 100%									
Listing first 45 summaries									
Database :	PIR_79;*								
	1: pir1;*								
	2: pir2;*								
	3: pir3;*								
	4: pir4;*								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Match Length	DB ID	Description					
1	516.5	83.7	118	S25174	Ig heavy chain V region - mouse	C;Species: Mus musculus (mouse, mouse)	C;Accession: S25174; S33133	R;Monastier, M.; Fasy, T.M.; Loeman, M.J.; Novick, K.E.; Muller, S.	A;Description: Structure and binding properties of monoclonal antibodies to core histone
2	500.5	81.1	136	S04576	Ig heavy chain pre	A;Reference number: S25174	A;Accession: S31333	A;Status: preliminary	A;Molecule type: mRNA
3	500	81.0	137	S52445	Ig heavy chain Vr	A;Residue: 1-118 <MON>	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
4	493	79.9	178	S29594	Ig gamma chain (W)	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
5	487.5	79.0	120	S03471	Ig heavy chain V-D	A;Residue: 1-118 <MON>	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
6	478	77.5	116	S15672	Ig heavy chain Vr	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
7	474.5	76.9	117	S17586	Ig heavy chain pre	A;Residue: 1-118 <MON>	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
8	474	76.8	122	S05623	Ig heavy chain Vr	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
9	470.5	76.3	115	S03482	Ig heavy chain V-D	A;Residue: 1-118 <MON>	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
10	460.5	74.6	121	S49220	Ig gamma-1 chain -	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
11	456.5	74.0	120	S03484	Ig heavy chain V-D	A;Residue: 1-118 <MON>	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
12	453.5	73.5	107	PH1013	Ig heavy chain Vr	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
13	453	73.4	268	A56446	Ig heavy chain Vr	A;Residue: 1-118 <MON>	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
14	451.5	73.2	115	S24289	Ig gamma chain Vr	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
15	446.5	72.4	233	JC5322	P53 specific singl	A;Residue: 1-118 <MON>	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
16	446	72.3	108	PH1012	Ig heavy chain Vr	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
17	445	72.3	115	PL0245	Ig heavy chain Vr	A;Residue: 1-118 <MON>	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
18	443	71.8	123	PH1403	Ig heavy chain Vr	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
19	442	71.6	118	A47267	Ig heavy chain Vr	A;Residue: 1-118 <MON>	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
20	439	71.2	114	A47271	Nitrophenyl phosph	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
21	436.5	70.7	249	S41374	Single chain Fv an	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
22	428	69.4	288	S29690	Ig heavy chain VH	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
23	426.5	69.1	119	E30562	Ig heavy chain VR	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
24	424.5	68.8	119	D30562	Ig heavy chain VR	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
25	424	68.8	119	C30562	Ig heavy chain VR	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
26	422.5	68.5	138	S21810	Ig heavy chain VR	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
27	420.5	68.2	246	S38950	Ig gamma chain - m	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
28	416	68.2	446	A47295	Ig gamma -a chain	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA
29	67.4	107	2	A27646	Ig heavy chain VR	A;Accession: S31333	A;Cross-references: EMBL:X67622; PIDN:951854; PIDN:CMA47880.1; PID:9938259	A;Status: preliminary	A;Molecule type: mRNA

C;Keywords: heterotetramer; immunoglobulin
 F;1-19/Domain: Signal sequence #status predicted <SIG>
 F;20-136/Domain: Ig heavy chain V region (fragment) #status predicted <MAT>
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 500.5; DB 2; Length 136;
 Best Local Similarity 83.8%; Pred. No. 1.8e-39; Matches 98; Conservative 4; Mismatches 14; Indels 1; Gaps 1; Status 1; Db S03445

RESULT 3

Ig heavy chain V region precursor - mouse
 CSpecies: Mus musculus (house mouse)
 CAccession: S03445
 CRBergdorff, J.; Kraehnholz, J.P.
 C;Description: Specific amplification by the polymerase chain reaction of rearranged genes submitted to the EMBL Library, November 1994
 A;Reference number: S52445
 A;Accession: S52445
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-137

 A;Cross-references: EMBL:X82690; NID:9673439; PIDN:CAA58011.1; PID:9673440
 A;Introns: 16/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 C;Genetics:
 C;Residues: 1-137

Query Match 81.0%; Score 500; DB 2; Length 137;
 Best Local Similarity 82.2%; Pred. No. 2e-39; Matches 97; Conservative 7; Mismatches 12; Indels 2; Gaps 1; Status 1; Db S03445

RESULT 4

Ig gamma chain (MM65) - mouse (fragment)
 CSpecies: Mus musculus (house mouse)
 C;Accession: S29594
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S29594
 CR;Seymour, R.
 C;Submitter to the EMBL Data Library, February 1991
 A;Reference number: S29593
 A;Accession: S29594
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-178 <SEY>
 A;Cross-references: EMBL:X57857; NID:952590; PIDN:CAA40992.1; PID:952591
 C;Keywords: immunoglobulin

Query Match 79.9%; Score 493; DB 2; Length 178;
 Best Local Similarity 80.5%; Pred. No. 1.2e-38; Matches 95; Conservative 8; Mismatches 13; Indels 2; Gaps 1; Status 1; Db S29594

RESULT 5

Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
 CSpecies: Mus musculus (house mouse)
 C;Accession: S03471; S07453
 CRocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Rougerau, M
 C;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not suggest a hypervariable region.
 A;Reference number: S03471; MUID:83058021; PMID:6815271
 A;Accession: S07453
 A;Molecule type: mRNA
 A;Residues: 1-43 <RO2>
 C;Superfamily: immunoglobulin V region; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 487.5; DB 2; Length 120;
 Best Local Similarity 79.8%; Pred. No. 2.5e-38; Matches 95; Conservative 8; Mismatches 13; Indels 3; Gaps 1; Status 1; Db S15672

RESULT 6

Ig heavy chain V region - mouse (fragment)
 CSpecies: Mus musculus (house mouse)
 C;Accession: S15672
 CR;Tempest, P.; Bremer, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris, P.; Technology, Bio 9, 266-271, 1991
 A;Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial virus
 A;Reference number: S15672; MUID:91337412; PMID:1367535
 A;Accession: S15672
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-116 <TEM>
 A;Cross-references: EMBL:X58835; NID:951978; PIDN:CAA16441; PID:951979
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 478; DB 2; Length 116;
 Best Local Similarity 78.3%; Pred. No. 1.8e-37; Matches 90; Conservative 9; Mismatches 16; Indels 0; Gaps 0; Status 1; Db S03471

RESULT 7

Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
 CSpecies: Mus musculus (house mouse)
 C;Accession: S03471; S07453
 CRocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Rougerau, M
 C;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not suggest a hypervariable region.
 A;Reference number: S03471; MUID:83058021; PMID:6815271
 A;Accession: S07453
 A;Molecule type: mRNA
 A;Residues: 1-43 <RO2>
 C;Superfamily: immunoglobulin V region; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 478; DB 2; Length 116;
 Best Local Similarity 78.3%; Pred. No. 1.8e-37; Matches 90; Conservative 9; Mismatches 16; Indels 0; Gaps 0; Status 1; Db S03471

QY 62 PNFQGRATMTADTSNTAYQLQLSLSITSEDAVYCYGGTTFAYWQGQITLVSA 116
 S17586 |||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Ig heavy chain V region (BB) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C;Accession: S17586
 A;Title: Biochemical implications from the variable gene sequences of an anti-cytochrome
 forms.
 A;Reference number: S17586; MUID:92015240; PMID:1656053
 A;Accession: S17586
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residue: 1-117 <MIL>
 A;Cross-references: EMBL:X0683; NID:951820; PIDN:CA443095.1; PID:951821
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 474.5; DB 2; Length 117;
 Best Local Similarity 77.5%; Pred. No. 3.9e-37;
 Matches 93; Conservative 10; Mismatches 10; Indels 7; Gaps 2;
 QY 61 APNFGQRATMTADTSNTAYQLQLSLSITSEDAVYCYGGTTFAYWQGQITLVSA 116
 61 DPKQDQKATITADTSNTAYQLQLSLSITSEDAVYCYGGTTFAYWQGQITLVSA 117

RESULT 8
 S06823 Ig heavy chain V region (clone IIC) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
 C;Accession: S06823
 R;Miller III, A.; Glazel, J.A.
 J. Mol. Biol. 209, 763-778, 1989
 A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mوت
 A;Reference number: S06815; MUID:90064531; PMID:255519
 A;Accession: S06823
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-122 <MIL>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 76.8%; Score 474; DB 2; Length 122;
 Best Local Similarity 77.9%; Pred. No. 4.5e-37;
 Matches 95; Conservative 8; Mismatches 13; Indels 6; Gaps 2;
 QY 1 EVOLQOSGABLVLGASVAKLCTASGFNIDKYYIH-WVKRPEQGLEWIGCIPENGTEY 59
 1 EVOLQOSGABLVLGASVAKLCTASGFNIDKYYIH-WVKRPEQGLEWIGCIPENGTEY 60

QY 60 YAENFGQRATMTADTSNTAYQLQLSLSITSEDAVYCYGGTTFAYWQGQITLVSA 114
 61 YDPKQDQKATITADTSNTAYQLQLSLSITSEDAVYCYGGTTFAYWQGQITLVSA 120

RESULT 9
 S04922 Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 A;Variety: strain BALB/C
 C;Accession: S04922
 Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
 C;Accession: S03482; S045453
 R;Rocca-Serra, J.; Matthees, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougeron, B.;
 EMBO J. 2, 867-872, 1983
 A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four
 hypervariable regions.
 A;Reference number: S03471; MUID:84057768; PMID:6416834
 A;Accession: S03482
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Accession: S07453
 A;Cross references: EMBL:X0219
 A;Note: this sequence was determined from the differentiated gene
 R;Rocca-Serra, J.; Mazlie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.;
 J. Immunol. 129, 2554-2558, 1982
 A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does
 A;Status: number: S07453; MUID:83058021; PMID:6815271
 A;Accession: S07453
 A;Status: preliminary
 A;Molecule type: protein
 A;Residue: 1-43 <ROC2>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 470.5; DB 2; Length 115;
 Best Local Similarity 77.1%; Pred. No. 8.9e-37;
 Matches 91; Conservative 8; Mismatches 15; Indels 1; Gaps 1;
 QY 61 APNFGQRATMTADTSNTAYQLQLSLSITSEDAVYCYGGTTFAYWQGQITLVSA 114
 61 DPKQDQKATITADTSNTAYQLQLSLSITSEDAVYCYGGTTFAYWQGQITLVSA 115

RESULT 10
 S49220 Ig gamma-1 chain - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
 C;Accession: S49220
 R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
 submitted to the EMBL Data Library, September 1994
 A;Description: Cloning and expression of a recombinant mouse Rab-fragment recogn
 A;Reference number: S49220
 A;Accession: S49220
 A;Molecule type: mRNA
 A;Residues: 1-221 <KIP>
 A;Cross-references: EMBL:237502; NID:9541778; PIDN:CA85732.1; PID:9541779
 A;Experimental source: strain Balb/C
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F;1-120/Domain: V region #status predicted <VRG>
 F;21-221/Domain: C region #status predicted <CRG>
 F;139-203/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 460.5; DB 2; Length 221;
 Best Local Similarity 75.0%; Pred. No. 1.5e-35;
 Matches 90; Conservative 12; Mismatches 13; Indels 5; Gaps 2;
 QY 1 EVOLQOSGABLVLGASVAKLCTASGFNIDKYYIH-WVKRPEQGLEWIGCIPENGTEY 60

Db 115 SA 116

Db 121 SS 122

Qy 61 APNFOGRATMTADTSNTAYLQLSSLTSEDTAVYCYC---YCGTIPAYWQSGTLTVNSA 116
 C;Species: Mus musculus (house mouse)
 A;Variety: strain BALB/C
 C;Accession: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000

RESULT 11
 S03484
 Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 A;Variety: strain BALB/C
 C;Accession: S03484; S07453
 R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougeron, M.
 ENO J., 2, 867-872, 1983
 A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT hypervariable regions
 A;Reference number: S03471; MUID:84057768; PMID:6416834
 A;Accession: S03484
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 10-120 <ROCL>
 A;Cross-references: EMBL:X07144
 A;Note: this sequence was determined from the differentiated gene
 R;Rocca-Serra, J.; Matthes, H.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougeron, M.; Reference number: S07453; MUID:83058021; PMID:6815271
 A;Accession: S07453
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-43 <ROCL>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 P;15-98/Domain: immunoglobulin homology <IMM>
 Best Local Similarity 75.6%; Pred. No. 1.9e-35;
 Matches 90; Conservative 8; Mismatches 18; Indels 3; Gaps 1;

Qy 1 EVOLQSGAEILVRSGASVSKLSCTAGFNFNDYIYHWVKORPQEGLWIGCIDPENGDEY 60
 Db 1 EVOLQSGAEILVRSGASVSKLSCTAGFNFNDYIYHWVKORPQEGLWIGCIDPENGDEY 60
 Qy 61 APNFOGRATMTADTSNTAYLQLSSLTSEDTAVYCYGMI---TFAVWQSGTLTVSA 116
 Db 61 APNFOGRATMTADTSNTAYLQLSSLTSEDTAVYCYGMI---TFAVWQSGTLTVSA 116
 61 GPKFOGKATTAIDTSNTAYLQLSSLTSEDTAVYCYGMI---TFAVWQSGTLTVSS 119
 RESULT 12
 PH1013
 Ig heavy chain V region (clone 111.67) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 A;Accession: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J;Exp. Med., 176, 761-779, 1992
 A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
 A;Reference number: PH0971; MUID:92381444; PMID:1512540
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-107 <TIL>
 A;Experimental source: B cell, strain [NZB x NWJ]F1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;15-98/Domain: immunoglobulin homology <IMM>
 Query Match 73.5%; Score 453.5; DB 2; Length 107;
 Best Local Similarity 83.2%; Pred. No. 3.1e-35; Indels 1; Gaps 1; Mismatches 89; Conservative 6; MisMatches 11;

Qy 1 EVOLQSGAEILVRSGASVSKLSCAGFNFNDYIYHWVKORPQEGLWIGCIDPENGDEY 60
 Db 1 EVOLQSGAEILVRSGASVSKLSCAGFNFNDYIYHWVKORPQEGLWIGCIDPENGDEY 60
 RESULT 13
 A56446
 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
 C;Species: Mus musculus (house mouse)
 C;Accession: A56446
 C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
 R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
 J; Biol. Chem. 270, 7229-7035, 1995
 A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical to the digoxin-binding protein from the heart muscle
 A;Reference number: A56446; MUID:95229583; PMID:7713873
 A;Accession: A56446
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-268 <TA>
 A;Cross-references: GB:U20617
 A;Keywords: heterotetramer; immunoglobulin
 Query Match 73.4%; Score 453; DB 2; Length 268;
 Best Local Similarity 76.3%; Pred. No. 9.2e-35; Mismatches 9; Indels 2; Gaps 1;
 Matches 90; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

Qy 1 EVOLQSGAEILVRSGASVSKLSCAGFNFNDYIYHWVKORPQEGLWIGCIDPENGDEY 60
 Db 3 QVQLQSGAEILVRSGASVSKLSCAGFNFNDYIYHWVKORPQEGLWIGCIDPENGDEY 60
 Qy 61 APNFOGRATMTADTSNTAYLQLSSLTSEDTAVYCYGMI---TFAVWQSGTLTVSA 116
 Db 63 DPKFOGKATTAIDTSNTAYLQLSSLTSEDTAVYCYGMI---TFAVWQSGTLTVSS 120
 RESULT 14
 S24289
 Ig gamma chain V region (JS34/32) - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
 R;Moncharmont, B.
 Submitted to the EMBL Data Library, September 1991
 A;Description: Cloning and sequencing of the cDNA coding for the variable regions of the Ig gamma chain
 A;Reference number: S24287
 A;Accession: S24289
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-116 <KON>
 A;Cross-references: EMBL:X62705; NID:951690; PID:CAA44584.1; PID:91333963
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;14-97/Domain: immunoglobulin homology <IMM>
 Query Match 73.2%; Score 451.5; DB 2; length 116;
 Best Local Similarity 75.2%; Pred. No. 5.2e-35; Mismatches 88; Conservative 13; Indels 3; Gaps 2;
 Matches 88; Conservative 13; Mismatches 13; Indels 3; Gaps 2;

Qy 2 VOLQSGAEILVRSGASVSKLSCAGFNFNDYIYHWVKORPQEGLWIGCIDPENGDEY 61
 Db 1 VOLQSGAEILVRSGASVSKLSCAGFNFNDYIYHWVKORPQEGLWIGCIDPENGDEY 60
 Qy 62 PNFOGRATMTADTSNTAYLQLSSLTSEDTAVYCYGMI---TFAVWQSGTLTVSA 116
 Db 61 PKFOGKATTAIDTSNTAYLQLSSLTSEDTAVYCYGMI---TFAVWQSGTLTVSS 116

RESULT 15
 JC522
 P53 specific single-chain antibody Fab421 - human
 C;Species: Homo sapiens (man)
 C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997

C;Accession: JCS322

R;Jannet, C.B.; Rynes, N.E.

Biochem. Biophys. Res. Commun. 230: 242-246, 1997

A;Title: Characterization of scFv421, a single-chain antibody targeted to p53.

A;Reference number: JCS322; MUID:97168950; PMID:9016757

A;Accession: JCS322

A;Molecule type: mRNA

A;Residues: 1-233 <JAN>

A;Experimental source: hydrioma cell

C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 72.4%; Score 446.5; DB 2; Length 233;

Best Local Similarity 77.7%; Pred. No: 3.2e-34; Matches 87; Conservative 7; Mismatches 15; Indels 3; Gaps 1;

QY 5 QOSGAELVRSAGASVULKSCSITASGFNIKDYIHWVKORPQQEGLWIGCIDPENGDTAYAPNE 64
Db 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65 QGRATMTADTSNTAYLQLSLTSEDTAVVTCYGGTTIFAYWGOQSPILVUTSA 116
Db 61 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GVKATWTADISSNTAYLQLSLTSEDTAVVTCNAG---MDYWGQITIVSS 109

Search completed: December 29, 2004, 18:06:56

Job time : 16.0782 secs

THIS PAGE BLANK (use reverse)

CC chosen from glomerulonephritis, scleroderma, multiple sclerosis, lupus
 CC nephritis, cirrhosis, atherosclerosis, inflammatory bowel disease or
 CC rheumatoid arthritis. The antibodies are also useful for treating
 CC oncogenic disease or cancer, Crohn's disease, diabetic nephropathy,
 CC cachexia, stroke, ulcerative colitis, coronary restenosis, Huntington's
 CC disease and parkinson's disease. The present sequence represents a murine
 XX monoclonal antibody (mab) IAI heavy chain variable region
 SQ Sequence 122 AA;

Query Match 87.0%; Score 537; DB 7; Length 122;
 Matches 16; Conservative 3; Mismatches 4; Indels 12; Gaps 2;

QY 1 EVOLQOSGABELVRSAGSVKLSCASGNKIDNYMHVKQRPEQGLEWIGIDPENGDTY 60
 Db 1 EVOLQOSGABELVRSAGSVKLSCASGNKIDNYMHVKQRPEQGLEWIGIDPENGDTY 60

QY 61 APNFQGRATMTADTSNTAYLQLSSLTSEDATAVYCVNTAWYGTSGG--FAWGQGTT 111
 Db 61 APKFQGKATMTADTSNTAYLQLSSLTSEDATAVYCVNTAWYGTSGG--FAWGQGTT 117

QY 112 VTVSA 116
 Db 118 VTVSS 122

RESULT 2
 ADQ31245
 ID ADQ31245 standard; protein: 122 AA.

AC ADQ31245;
 XX
 DT 09-SEP-2004 (first entry)

DB Murine IAI heavy chain variable domain antibody protein SeqID 11.
 XX
 KW murine; IAI; monocyte chemotactic protein; beta-chemokine family; MCP-3;
 KW glomerulonephritis; scleroderma; cirrhosis; multiple sclerosis;
 KW lupus nephritis; atherosclerosis; inflammatory bowel disease;
 KW rheumatoid arthritis; inflammatory disease; fibrotic disorder; cancer;
 KW immunopathological disorder; antiarteriosclerotic; antiarthritic;
 KW anti-inflammatory; antirheumatic; cytotatic; dermatological;
 KW hepatotropic; immunomodulator; nephrotropic; neuroprotective; mouse; MCP.
 OS Mus musculus.

XX
 PD 17-JUN-2004.
 XX
 PP 25-NOV-2003; 2003WO-US037834.
 XX
 PR 27-NOV-2002; 2002US-0430007P.
 XX
 PA (BIOG-) BIOPHARMA INC.
 XX
 PI De Fougerolles AR, Kotelianski VE, Garber E, Reid C, Saldanha JW;
 Van Vlijmen H;
 WPI; 2004-461110/43.

XX
 DR N-PSDB; ADQ31243.
 XX
 PT New antibodies against monocyte chemotactic protein (MCP), useful for
 PT treating or preventing disorders associated with detrimental MCP
 activity, e.g. glomerulonephritis, scleroderma, multiple sclerosis, or
 atherosclerosis.

XX
 PS Example 9; SEQ ID NO 11; 200pp; English.

This invention relates to an antibody for treating or preventing monocyte chemotactic protein (MCP) activity. Specifically, it refers to humanised antibodies that bind to

CC members of the beta-chemokine family (of which MCP-1, MCP-2 and MCP-3
 CC belong) and in particular antibodies that have been modelled on, and
 CC modified from, the variable complementary determining regions (CDRs) of
 CC the murine IAI and IAI immunoglobulin sequences. The present invention
 CC describes using these antibodies to treat or prevent diseases and
 CC disorders including glomerulonephritis, scleroderma, cirrhosis, multiple
 CC sclerosis, lupus nephritis, atherosclerosis, inflammatory bowel diseases,
 CC rheumatoid arthritis, inflammatory diseases, fibrotic disorders, cancer
 CC and immunopathological disorders. Accordingly, they can be used in the
 CC development of pharmaceutical compositions that exhibit
 CC cytostatic, dermatological, hepatotropic, immunomodulator, nephrotropic
 CC and neuroprotective activities. This polypeptide sequence is the murine
 XX IAI heavy chain antibody protein of the invention.

SQ Sequence 122 AA;

Query Match 87.0%; Score 537; DB 8; Length 122;
 Matches 16; Conservative 3; Mismatches 4; Indels 12; Gaps 2;

QY 1 EVOLQOSGABELVRSAGSVKLSCASGNKIDNYMHVKQRPEQGLEWIGIDPENGDTY 60
 Db 1 EVOLQOSGABELVRSAGSVKLSCASGNKIDNYMHVKQRPEQGLEWIGIDPENGDTY 60

QY 61 APNFQGRATMTADTSNTAYLQLSSLTSEDATAVYCVNTAWYGTSGG--FAWGQGTT 111
 Db 61 APKFQGKATMTADTSNTAYLQLSSLTSEDATAVYCVNTAWYGTSGG--FAWGQGTT 117

QY 112 VTVSA 116
 Db 118 VTVSS 122

RESULT 3
 ADQ31245
 ID ADQ31245 standard; protein: 122 AA.

AC ADQ31245;
 XX
 DT 09-SEP-2004 (first entry)

DB Humanised murine IAI heavy chain antibody protein SeqID 51.
 XX
 KW IAI; monocyte chemotactic protein; beta-chemokine family;
 KW glomerulonephritis; scleroderma; cirrhosis; multiple sclerosis;
 KW lupus nephritis; atherosclerosis; inflammatory bowel disease;
 KW rheumatoid arthritis; inflammatory disease; fibrotic disorder; cancer;
 KW immunopathological disorder; antiarteriosclerotic; antiarthritic;
 KW anti-inflammatory; antirheumatic; cytotatic; dermatological;
 KW hepatotropic; immunomodulator; nephrotropic; neuroprotective; mouse; MCP;
 KW murine; humanised antibody.

XX
 OS Mus musculus.
 OS Synthetic.

XX
 PN WO2004050836-A2.
 XX
 DD 17-JUN-2004.

XX
 PP 25-NOV-2003; 2003WO-US037834.
 XX
 PR (BIOG-) BIOPHARMA INC.

XX
 PI De Fougerolles AR, Kotelianski VE, Garber E, Reid C, Saldanha JW;
 Van Vlijmen H;
 WPI; 2004-461110/43.

XX
 PT New antibodies against monocyte chemotactic protein (MCP), useful for
 PT treating or preventing disorders associated with detrimental MCP
 activity, e.g. glomerulonephritis, scleroderma, multiple sclerosis, or
 atherosclerosis.

XX
 PS Example 9; SEQ ID NO 11; 200pp; English.

This invention relates to an antibody for treating or preventing monocyte chemotactic protein (MCP) activity. Specifically, it refers to humanised antibodies that bind to

CC members of the beta-chemokine family (of which MCP-1, MCP-2 and MCP-3
 CC belong) and in particular antibodies that have been modelled on, and
 CC modified from, the variable complementary determining regions (CDRs) of
 CC the murine IAI and IAI immunoglobulin sequences. The present invention
 CC describes using these antibodies to treat or prevent diseases and
 CC disorders including glomerulonephritis, scleroderma, cirrhosis, multiple
 CC sclerosis, lupus nephritis, atherosclerosis, inflammatory bowel diseases,
 CC rheumatoid arthritis, inflammatory diseases, fibrotic disorders, cancer
 CC and immunopathological disorders. Accordingly, they can be used in the
 CC development of pharmaceutical compositions that exhibit
 CC cytostatic, dermatological, hepatotropic, immunomodulator, nephrotropic
 CC and neuroprotective activities. This polypeptide sequence is the murine
 XX IAI heavy chain antibody protein of the invention.

PT activity, e.g. glomerulonephritis, scleroderma, multiple sclerosis, or atherosclerosis.

PT

XX

PS

CC Disclosure; SEQ ID NO 51; 200pp; English.

CC This invention relates to an antibody for treating or preventing disorders associated with detrimental monocyte chemoattractant protein (MCP) activity. Specifically, it refers to humanised antibodies that bind to members of the beta-chemokine family (of which MCP-1, MCP-2 and MCP-3 belong) and in particular antibodies that have been modelled on, and modified from, the variable complementarity determining regions (CDRs) of the murine 1A2 and 1A1 immunoglobulin sequences. The present invention describes using these antibodies to treat or prevent diseases and disorders including glomerulonephritis, scleroderma, cirrhosis, multiple sclerosis, lupus nephritis, atherosclerosis, inflammatory bowel diseases, rheumatoid arthritis, inflammatory diseases, fibrotic disorders, cancer and immunopathological disorders. Accordingly, they can be used in the development of pharmaceutical compositions that exhibit antiarteriosclerotic, antiarrhythmic, antiinflammatory, antirheumatic, cytostatic, dermatological, hepatotropic, immunomodulator, nephroprotective and neuroprotective activities. This polypeptide sequence is the humanised murine 1A1 variable and constant heavy chain antibody protein of the invention.

CC

XX

SQ Sequence 122 AA;

Query Match 85.6%; Score 528; DB 8; Length 122;
Best Local Similarity 85.2%; Pred. No. 2.5e-40; Matches 104; Conservative 2; Mismatches 4; Indels 12; Gaps 2;

QY 1 EVOLQOSGALVRSAGSVKLSCTASGPNIKYIHWKQRPEQGLEWIGCIDPENGDTY 60
Db 1 EVQLOQSGALVRSAGSVKLSCTASGPNIKYIHWKQRPEQGLEWIGIDPENGDTY 60
QY 61 APNFGQRAITMDATSSNTAYLQLSSLTSEBDTAVYTC--YGGTTTFAWMQGQTLY 111
Db 61 APKFQGKATWMDATSSNTAYLQLSSLTSEBDTAVYTC--YGGTTTFAWMQGQTLY 111
QY 112 VT 113
Db 118 VT 119

RESULT 4

AAW0769

ID AAW0769 standard; protein; 243 AA.

XX

AC AAW0769;

XX

DT 08-SEP-1998 (first entry)

XX

DB Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.

XX

KW Single chain antibody (ScFv) 421; mouse; p53 protein; oligomerisation; regulatory domain; p53 mutant; H273; W248; G281; p53-dependent trans-activating activity; restoration; tumour-suppressing activity; tumour cell; treatment; hyper-proliferation; cancer; re-stenosis; BB.

XX

OS Mus sp.

XX

PN WO9818825-A1.

XX

PR 29-OCT-1996; 96FR-00013176.

XX

PA (RION) RHONE-POULENC RORER SA.

XX

PI Bracco L, Debuschle L;

XX

DR WPI; 1998-272140/24.

DR N-PSDB; AAV36236.

XX

PT Restoring p53-dependent trans-activating activity to cell containing mutant p53 - by delivering single-chain antibody specific for the mutant, particularly for treatment of tumours.

XX

PS Claim 5; Page 31; 54pp; French.

CC

CC The present sequence represents a single chain antibody (ScFv) designated 421. The antibody binds to an epitope present in the C-terminal region of the p53 protein that includes oligomerisation and regulatory domains, specifically between positions 320 and 393. ScFv 421 is directed against p53 mutants particularly H273, W248 and G281 mutants. When the ScFv is introduced into cells containing a mutant p53 protein, p53 dependent trans-activating activity is restored. ScFv 421 is specific for p53-mutants that have lost tumour-suppressing activity and are present in tumour cells. It is particularly used to treat hyper-proliferation associated with these mutants (e.g. cancer and re-stenosis) but may also be used in vitro for studying mechanisms of activity of p53 or its mutant and to purify or detect p53

XX

SQ Sequence 243 AA;

Query Match 85.3%; Score 526; DB 2; Length 243;
Best Local Similarity 86.4%; Pred. No. 8.1e-40; Matches 102; Conservative 5; Mismatches 7; Indels 4; Gaps 2;

QY 1 EVOLQOSGALVRSAGSVKLSCTASGPNIKYIHWKQRPEQGLEWIGCIDPENGDTY 60
Db 1 EVOLQOSGALVRSAGSVKLSCTASGPNIKYIHWKQRPEQGLEWIGIDPENGDTY 60
QY 61 APNFGQRAITMDATSSNTAYLQLSSLTSEBDTAVYTC--YGGTTTFAWMQGQTLY 116
Db 61 APKFQGKATWMDATSSNTAYLQLSSLTSEBDTAVYTC--YGGTTTFAWMQGQTLY 116

RESULT 5

AAW01585

ID AAW01586 standard; protein; 118 AA.

XX

AC AAW01586;

XX

DT 22-AUG-1997 (first entry)

XX

DB Lead binding MAb 14G11 heavy chain variable region.

XX

KW Monoclonal antibody; Ed fragment; lead cation; perfume; cosmetic; pharmaceutical; health care; skin treatment; pesticide; herbicide; heavy metal.

XX

OS Mus musculus.

XX

PN WO9539518-A1.

XX

PD 12-DEC-1996.

XX

PP 05-JUN-1996; 96WO-US009258.

XX

PR 05-JUN-1995; 95US-00462798.

XX

PR 10-OCT-1995; 95US-00541373.

XX

PA (BION-) BIONEBRASKA INC.

XX

PI Wyile DE, Lopez O, Murray PJ;

XX

DR WPI; 1997-03140/04.

DR N-PSDB; AAT58260.

XX

PT DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as lead

XX

PT detections.

XX

PS Claim 12; Page 75; 125pp; English:

卷之三

The present sequence represents the heavy chain variable region for monoclonal antibody (Mab) 14G11, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from mouse hybridoma cells. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of specific heavy metals.

PT autoimmune response to the C-terminal DNA-binding domain of the p53 or PT protein by an active compound comprising of antibodies to p53 or PT fragments of p53.

XX

PS Claim 78; Fig 9; 87pp; English.

CC domain deleted and replaced by a leucine zipper domain. The mutants
CC preferably also have at least part of the p53 transactivating domain
(amino acids 1-74) deleted and replaced by the transactivating domain
(TD) from herpes simplex virus viral protein VP16 (amino acids 411-490)
or by a protein domain able to bind selectively to a transactivator,
especially a single-chain antibody variable domain, (ScFv). The present
CC sequence is that of a specifically claimed p53 variant designated S-225
CC and comprising a ScFv domain, amino acids 75-325 of human wild-type p53
and a leucine zipper domain at the C-terminal. The p53 variants are more
active and more stable tumour suppressors and apoptosis-inducing agents
CC than wild-type p53 and are active where the wild-type protein is not,
i.e. they are not inactivated by dominant negative or oncogenic mutants,
CC nor by other cellular proteins (because the leucine zipper domain
CC prevents formation of inactive mixed oligomers)

Sequence 535 AA;

Query Match 83.6%; Score 516; DB 2; Length 535;
Matches 100; Conservative 6; Mismatches 8; Indels 4; Gaps 2;

Qy 1 EVQLQSGAELVRSAGSVKLSCTASGFNKDYIHWVKRPEQGLEWIGCIDPENGTEY 60
Db 3 QVOLQSGAELVRSAGSVKLSCTASGFNKDYIHWVKRPEQGLEWIGCIDPENGTEY 62
Qy 61 APNFGGRATMTADTSNTAYLQLSSLTSEDAVYTC--YGGTITFAWMGGTLTVSA 116
Db 63 APKFQSKATMTADTSNTAYLQLSSLASEDAVYTCNFYGDALD--YWGQGTIVVSS 118

RESULT 8

AAW28492 standard; protein; 535 AA.

AC AAW28492;

XX DT 25-NOV-1997 (first entry)
XX DB Human p53 protein variant S-325H.

XX KW Leucine zipper domain; I2D; oligomerisation domain; mutant; mutein;
KW substitution; replacement; transactivation; viral protein VP16; HSV;
KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
KW tumour suppression; apoptosis; single chain antibody variable domain.
XX OS Homo sapiens.
OS Herpes simplex virus.
OS Synthetic.
OS Chimeric.

FH Location/Qualifiers
FT Key 36.1
FT /note= "Arg residue at position 182 of wild-type p53 has
FT been mutated to His"
FT WO9704092-A1.XX DT 06-FEB-1997.
XX PP 17-JUL-1996; 96W0-FR00111.
XX PR 19-JUL-1995; 95FR-00008729.
XX PA (RHON) RHONE POULENC RORER SA.
XX PI Conseiller E, Bracco L;

XX DR WPI; 1997-132633/12.

XX PT New p53 variants e.g. with oligomerisation domain replaced by leucine
PT zipper - useful for treating hyper-proliferative disorders, esp. cancer
PT and restenosis.

PS Claim 36; Page: 133pp; French.

CC XX Query Match 83.6%; Score 516; DB 2; Length 535;
CC Matches 100; Conservative 6; Mismatches 8; Indels 4; Gaps 2;
CC Sequence 535 AA;
CC XX ID ABB99635 standard; protein; 119 AA.
CC AC ABB99635;
CC XX DT 28-MAR-2003 (first entry)
CC DB 2A2 monoclonal antibody heavy chain variable region.
CC XX KW Heavy chain; variable region; monoclonal antibody; 2A2; cathepsin B;
CC cancer; arthritis.
CC OS Mus sp.
CC XX PN WO200294881-A2.
CC PD 28-NOV-2002.
CC PF 02-APR-2002; 2002WO-SI000013.
CC XX PR 18-MAY-2001; 2001SI-00000132.
CC XX PA (KRKA) KRKA TOVARNA ZDRAVIL DD.
CC XX PI Kos J, Premzl A, Kopitar Jerala N, Fan X, Turk V, Bestagno M;
CC PI Burrone OR;
CC XX DR WPI; 2003-120791/11.
CC DR N-FSDB; ABV77141.
CC PT New neutralizing antibodies directed against Cathepsin B, useful for
CC PT treating and/or diagnosing a disease associated with an increased
CC PT cathepsin B activity or concentration, e.g. cancer or arthritis.
CC XX PS Claim 3; Fig 6; 44pp; English.

CC XX The present sequence represents the heavy chain variable region of the

CC murine monoclonal antibody 2A2. 2A2 is a neutralising antibody which is directed against cathepsin B. The antibody is useful for treating and diagnosing a disease associated with an increased cathepsin B activity, such as cancer or arthritis. The antibody is also useful for manufacturing a medicament for treating or diagnosing these diseases.

Sequence 119 AA;

Query Match 83.4%; Score 514.5; DB 6; Length 119;
Best Local Similarity 83.2%; Pred. No. 4.1e-39; Mismatches 99; Conservative 6; Indels 11; Gaps 3; Sequence 119 AA;

Matched sequence:

```
1 EVOLQSGAEVLRSAGSALKSCTASGNIKDYYHMKRQRPEQLEWIGCIDIIDENGDTY 60
  1 QVOLQSGAEVLRSAGSALKSCTASGNIKDYYHMKRQRPEQLEWIGCIDIIDENGDTY 60
  1 LOQSGAEVLRSAGSALKSCTASGNIKDYYHMKRQRPEQLEWIGCIDIIDENGDTY 60
```

Query 61 APNFORATMADTSNTAYLQLSSLTSEDATAVYCYG--GTTFAYWQGQTLYTVA 116
DB 61 APKFRGKATMTADTSNTAYLQLSSLTSEDATAVYCNARRHGYEMDYWGQGTSVTVSS 119

RESULT 10

RAW89173

AAW89173 standard; peptide; 112 AA.

AC AAW89173;

XX DT 25-MAR-1999 (first entry)

DE DE Anti-p53 monoclonal antibody 421 variable heavy chain sequence.

KW KW immune response; tumour associated antigen; metastatic cancer.

OS OS Mus sp.

XX Synthetic.

PN PN WO9856416-A1.

XX PD 17-DEC-1998.

XX PR 03-JUN-1998; 98WO-IL000266.

PR 09-JUN-1997; 97IL-00121041.

XX PA (YEDA) YEDA RES & DEV CO LTD.

PI PI Cohen IR, Rotter V, Wolkowicz R, Ruiz PJ, Brez-Alon N, Herkel J;

DR DR XX WPI; 1999-070296/06.

PT PT Use of a monoclonal antibody to a tumour-associated antigen - to induce anti-tumour immunity or elicit an increased immune response to the antigen.

XX PS Example 3; Fig 3; 47pp; English.

XX CC The present invention describes the use of an immunogen (A) to induce anti-tumour immunity; to elicit an increased immune response to tumour associated antigen (TAA) and/or to induce an immune response to mutant or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody (Mab) to TAA, or its fragment; (ii) a peptide based on a CDR (complementarity determining region) on the heavy or light chain of Mab (able to elicit antibodies to TAA); or (iii) a DNA that encodes the variable (V) region of Mab, in a gene delivery vehicle. The present sequence represents the variable heavy chain sequence from anti-p53 Mab 421. Also described is a method for generating sequence-specific, anti-DNA antibodies (Ab), by immunising a mammal with a Mab directed to a domain containing a DNA-binding site of a DNA-binding protein. (A) is used to treat a wide variety of primary and metastatic cancers, particularly those where p53 is involved. Ab are used for diagnosis (e.g. to determine critical sequences in animal or plant breeding; to identify bacteria and other parasites; to determine parentage; in forensic science

CC ; to isolate specific genes for DNA vaccination; in gene sequencing and cloning; also possibly for activation of selected therapeutic genes in plants, animals and humans. (A) induce an effective anti-tumour response without causing harm to the patient. The method uses (A) to generate anti-CC -TAA by exploiting the anti-idiotypic network.

SQ Sequence 112 AA;

Query Match 82.8%; Score 511; DB 2; Length 112;
Best Local Similarity 86.8%; Pred. No. 8e-39; Mismatches 99; Conservative 4; Indels 7; Gaps 4; Sequence 112 AA;

Matched sequence:

```
4 LQSGNLVLSGASTKLSTASGNIKDYYHMKRQRPEQLEWIGCIDIIDENGDTY 63
  1 LOQSGNLVLSGASTKLSTASGNIKDYYHMKRQRPEQLEWIGCIDIIDENGDTY 63
  1 LOQSGNLVLSGASTKLSTASGNIKDYYHMKRQRPEQLEWIGCIDIIDENGDTY 63
```

Query 64 FQGRATMADTSNTAYLQLSSLTSEDATAVYCYG--YCTTITAYWQGTLVVS 115
DB 61 FQGKATMTADTSNTAYLQLSSLTSEDATAVYCNPYDALD--YWGGTTVVS 112

RESULT 11

AAR60566

AAW60566 standard; protein; 124 AA.

ID AAR60566;

XX AC AAR60566;

XX DT 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 25-APR-1995 (first entry)

XX DE DE Anti-carcinoembryonic antigen chimeric heavy chain Ab.

XX KW KW chimeric human-murine; breast or colorectal carcinoma; heavy chain.

XX OS OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

XX PN PN WO9419466-A2.

XX PR 01-SEP-1994.

XX PR 16-FEB-1994; 94WO-US001709.

XX PR 16-FEB-1993; 93US-00017570.

XX PA (DOWC) DOW CHEM CO.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Gourlie BB, Rixon MW, Mezes PS, Kaplan DA, Schliom J;

DR DR N-PSD; AUQ71396.

XX PT Anti-carcinoembryonic antigen chimeric antibodies - for diagnosis and therapy of carcinoma, e.g. breast or colorectal carcinoma.

XX BS Claim 14; Page 53; 67pp; English.

XX CC AAQ71396 codes for AAR60566 the antibody heavy chain region of murine-human anti-carcinoembryonic antigen (CEA) chimeric antibody. Which can be used in *in vitro* immunoassays for the detection of CEA, and monitoring of tumour-associated antigen during therapy. It can also be used *in vivo* diagnostically, or in therapy for the treatment of tumours associated with colorectal and breast carcinomas, as well those of the gastrointestinal tract, lung, ovary and pancreas. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)

SQ Sequence 124 AA;

Query Match 82.3%; Score 508; DB 2; Length 124;

Best Local Similarity 81.5%; Pred. No. 1.7e-38; Matches 101; Conservative 4; Mismatches 11; Indels 8; Gaps 2;

QY 1 EVOLQSGAELVRSGASVULKSTAGNICKYIHWKQRPQGLEWIGCIPDENGTEY 60
Db - 1 EVOLQSGAELVRSGASVULKSTAGNICKYIHWKQRPQGLEWIGCIPDENGTEY 60

QY 61 APNFQGRATMTADTSNTAYQLQSSLISDTAVYTC---YGGTIT---FAYWGQGT 112
Db 61 APKFQGRATMTADTSNTAYQLQSSLISDTAVYTC---YGGTIT---FAYWGQGT 120

QY 113 TVSA 116
Db 121 TVSS 124

RESULT 12
ADH77307 ID ADH77307 standard; protein; 266 AA.

AC AC
XX XX

DT DT-APR-2004 (first entry)

DB Yeast killer toxin related anti-idiotypic scfv (H20).

XX variable region; anti-idiotypic antibody; yeast killer toxin; microbial infection; viral infection; candidosis; aspergillosis; cryptococcosis; sporotrichosis; histoplasmosis; thrush; tuberculosis; mycobacteriosis; respiratory infection; scarlet fever; pneumonia; impetigo; rheumatic fever; sepsis; septicaemia; cutaneous leishmaniasis; visceral leishmaniasis; keratitis; cystic fibrosis; typhoid fever; gastritis; flu; influenza; HIV; AIDS; H20.

XX OS Unidentified.

XX Key Location/Qualifiers
PH Misc-difference 126
FT /note= "Encoded by TTC"
XX WO2003095493-A2.

XX PD 20-NOV-2003.

XX PP 09-MAY-2003; 2003WO-IB002348.

PR 10-MAY-2002; 2002GB-00010783.

XX PA (UYSI-) UNIV SIENA.
PA (POLO/) ROLONELLI L.
PA (CASS/) CASSONE A.

XX PI Polonelli L, Cassone A;
XX DR WPI; 2004-012091/01.
DR N-RPSB; ADH77306.

XX PT New toxin-related polypeptides comprising a fragment of a variable region of an anti-idiotype antibody which recognizes the idiootope of an antibody specific for a yeast killer toxin, useful for treating microbial infections.

PT Disclosure; SEQ ID NO 22; 70pp; English.

CC The invention comprises a polypeptide which contains a part of the variable region of an anti-idiotypic antibody which recognizes the idiootope of an antibody specific for a yeast killer toxin. The polypeptide of the invention is useful for the treatment of microbial and viral infections, such as: candidosis, aspergillosis, cryptococcosis, sporotrichosis, blastomycosis, histoplasmosis, thrush, tuberculosis, mycobacteriosis, respiratory infections, scarlet fever, impetigo, rheumatic fever, sepsis, septicemia, cutaneous and visceral

CC leishmaniasis, keratitis, cystic fibrosis, typhoid fever, gastroenteritis and haemolytic-uremic syndrome, flu, influenza or HIV/AIDS. The present invention.

CC amino acid sequence represents an anti-idiotypic antibody (H20) of the invention.

SQ Sequence 266 AA;

Query Match 82.0%; Score 506; DB 8; Length 266;
Matches 98; Conservative 7; Mismatches 11; Indels 10; Gaps 2;

QY 1 EVOLQSGAELVRSGASVULKSTAGNICKYIHWKQRPQGLEWIGCIPDENGTEY 60
Db 3 OVOLOGSGAKLVRSGASVULKSTAGNICKYIHWKQRPQGLEWIGCIPDENGTEY 62

QY 61 APNFQGRATMTADTSNTAYQLQSSLISDTAVYTC---YGGTIT---FAYWGQGT 110
Db 63 APKFQGRATMTADTSNTAYQLQSSLISDTAVYTC---YGGTIT---FAYWGQGT 122

QY 111 TVSA 116
Db 123 TVCSS 128

RESULT 13
ID AAW41387 standard; protein; 120 AA.

XX AC AAW41387;
XX DT 02-JUN-1998 (first entry)

XX PR Anti-CEA antibody 806.077 heavy chain variable region.

XX PR Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy; cancer diagnosis; complementarity determining region; heavy chain.

XX OS Synthetic.

XX PN W09742329-A1.

XX PD 13-NOV-1997.

XX PR 29-APR-1997; 97WO-GB001165.

XX PR 04-MAY-1996; 96GB-00009405.

PR 14-FEB-1997; 97GB-00003103.

PA (ZENE) ZENECA LTD.

XX PI Copley CG, Edge MD, Emery SC;
XX DR WPI; 1997-558987/51.
DR N-PSPB; AAV1269.

XX PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis and therapy of cancer.

XX PS Claim 3; Page 196; 208pp; English.

This sequence is the heavy chain variable region of the antibody of the invention. The antibody is an anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab). Host cells or transgenic organisms transformed with DNA encoding the antibody, are used to make the antibody or conjugate. The conjugate is used in a medicament suitable for intravenous administration. The conjugate can be used for cancer therapy, selectively killing tumour cells. The antibody can be used for in vivo or in vitro diagnosis of cancer.

SQ Sequence 120 AA;

Query Match 81.8%; Score 505; DB 2; Length 120;
Best Local Similarity 80.8%; Pred. No. 3e-38;

RESULT 14
 QY 1 EVLOQSGAELVRSGASKLSCSTASGPNIKOYIHWVKORPEQLEWIGCIDPENGDTY 60
 DB 1 EVLOQSGAELVRSGASKLSCSTASGPNIKOYIHWVKORPEQLEWIGCIDPENGDTY 60
 QY 61 APNFGQRATMADTSNTAYQQLSSITSEDTAVYVC---YGGTTFAYWGOGLTVSA 116
 DB 61 APKFRGKATLTADSSNTAYLHLLSLTSEDTAVYCHVLIVAGYLAMDYWGQTSVAVSS 120

RESULT 15
 QY 1 EVLOQSGAELVRSGASKLSCSTASGPNIKOYIHWVKORPEQLEWIGCIDPENGDTY 60
 ID AAW82744 standard; protein; 281 AA.
 DE AAW82744;
 AC AAW82744;
 DT 10-MAY-1999 (first entry)
 DE Fusion protein pIC126/8061bcFvtag/mis.

KW Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein; prodrug-converting enzyme; cell surface antigen; treatment; cancer; inflammation; rheumatoid arthritis; antibody; prodrug therapy system.

XX OS Synthetic.
 XX PN WO851787-A2.
 XX PD 19-NOV-1998.
 XX PR 05-MAY-1998; 98WO-GB001294.
 PR 10-MAY-1997; 97GB-00009421.

XX PA (ZENE) ZENECA LTD.
 XX PI Emery SC, Blakey DC;
 XX DR WPI; 1999-059700/05.
 XX N-PSDB; AAV72069.

XX PT New gene construct expressing conjugate of targetting agent and prodrug-converting enzyme - useful for, e.g. targetted production of cytotoxic drug in vivo, especially for treatment of cancer.

XX Example 16; Page 84-85; 10pp; English.
 CC This sequence is a used in a method for obtaining a novel gene construct (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-targeting group (1) and a heterologous prodrug-converting enzyme (II), and (B) is directed to leave the cell for selective localisation at a cell surface antigen (Ag) recognised by (1). Delivery of (A) to a target site, then administration of (III) is used for targeted release of cytotoxic drug, specifically for treating cancer but also inflammation such as rheumatoid arthritis. In situ generation of the targeting antibody increases selectivity, reducing side effects at normal tissue. The method is applicable to any antibody-directed enzyme prodrug therapy.

CC Sequence 281 AA;
 CC Query Match 81.8%; Score 505; DB 2; length 281;
 CC Best Local Similarity 80.8%; Pred. No. 7.8e-38;
 CC Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVLOQSGAELVRSGASKLSCSTASGPNIKOYIHWVKORPEQLEWIGCIDPENGDTY 60
 DB 20 EVLOQSGAELVRSGASKLSCSTASGPNIKOYIHWVKORPEQLEWIGCIDPENGDTY 79
 QY 61 APNFGQRATMADTSNTAYQQLSSITSEDTAVYVC---YGGTTFAYWGOGLTVSA 116
 DB 80 APKFRGKATLTADSSNTAYLHLLSLTSEDTAVYCHVLIVAGYLAMDYWGQTSVAVSS 139

RESULT 14
 QY 1 EVLOQSGAELVRSGASKLSCSTASGPNIKOYIHWVKORPEQLEWIGCIDPENGDTY 60
 ID AAW41394 standard; protein; 255 AA.
 DE AAW41394;
 AC AAW41394;
 DT 17-OCT-2003 (revised)
 DE 02-JUN-1998 (first entry)
 Chimeric anti-CEA antibody 806.077 Hu IgG2 Fd chain.
 KW Anti-CEA antibody; carnoembryonic antigen; 806.077 Ab; cancer therapy; cancer diagnosis; complementarity determining region; Fd chain.
 XX OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 PN WO742329-A1.
 PD 13-NOV-1997.
 XX PR 97WO-GB001165.
 PR 04-MAY-1996; 96GB-00009405.
 PR 14-FEB-1997; 97GB-00003103.
 PR (ZENE) ZENECA LTD.
 XX PI Copley CG, Edge MO, Emery SC;
 XX DR WPI; 1997-558887/51.
 DR N-PSDB; NAV17291.
 XX PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis and therapy of cancer.
 XX PS Example 8; Page 102-103; 208pp; English.

This sequence is the HurgG2 Fd chain region of the antibody of the invention. The antibody is an anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab). Host cells or transgenic organisms transformed with DNA encoding the antibody, are used to make the antibody or conjugate. The conjugate is used in a medicament suitable for intravenous administration. The conjugate can be used for cancer therapy selectively killing tumour cells. The antibody can be used for in vivo or in vitro diagnosis of cancer. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 255 AA;

RESULT 15
 QY 1 EVLOQSGAELVRSGASKLSCSTASGPNIKOYIHWVKORPEQLEWIGCIDPENGDTY 60
 DB 20 EVLOQSGAELVRSGASKLSCSTASGPNIKOYIHWVKORPEQLEWIGCIDPENGDTY 79
 QY 61 APNFGQRATMADTSNTAYQQLSSITSEDTAVYVC---YGGTTFAYWGOGLTVSA 116
 DB 83 APKFRGKATLTADSSNTAYLHLLSLTSEDTAVYCHVLIVAGYLAMDYWGQTSVAVSS 142

Search completed: December 29, 2004, 17:57:29
 Job time : 82.7286 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 18:05:34 ; Search time 67.0678 Seconds
Sequence: 1 EVOLQOSGAEVLVRSGASVKL.....YGGTTIPAYWGGTIVTVSA 116
Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Title: US-10-774-076-4
Perfect score: 617

Sequence: 1 EVOLQOSGAEVLVRSGASVKL.....YGGTTIPAYWGGTIVTVSA 116
622.182 Million cell updates/sec

Searched: 1599051 Beqbs, 35972771 residues
Total number of hits satisfying chosen parameters: 1599051
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgm2_6/prodata/2/pubpaas/US07_PUBCOMB.pep:
2: /cgm2_6/prodata/2/pubpaas/US08_PUBCOMB.pep:
3: /cgm2_6/prodata/2/pubpaas/US09_PUBCOMB.pep:
4: /cgm2_6/prodata/2/pubpaas/US06_PUBCOMB.pep:
5: /cgm2_6/prodata/2/pubpaas/US07_PUBCOMB.pep:
6: /cgm2_6/prodata/2/pubpaas/US05_PUBCOMB.pep:
7: /cgm2_6/prodata/2/pubpaas/US08_NEW_PUB.PEP:
8: /cgm2_6/prodata/2/pubpaas/US08_PUBCOMB.pep:
9: /cgm2_6/prodata/2/pubpaas/US09_PUBCOMB.pep:
10: /cgm2_6/prodata/2/pubpaas/US09_NEW_PUB.PEP:
11: /cgm2_6/prodata/2/pubpaas/US09_PUBCOMB.pep:
12: /cgm2_6/prodata/2/pubpaas/US09_NEW_PUB.PEP:
13: /cgm2_6/prodata/2/pubpaas/US10_PUBCOMB.pep:
14: /cgm2_6/prodata/2/pubpaas/US10C_PUBCOMB.pep:
15: /cgm2_6/prodata/2/pubpaas/US10C_PUBCOMB.pep:
16: /cgm2_6/prodata/2/pubpaas/US10_PUBCOMB.pep:
17: /cgm2_6/prodata/2/pubpaas/US10_NEW_PUB.PEP:
18: /cgm2_6/prodata/2/pubpaas/US11_PUBCOMB.pep:
19: /cgm2_6/prodata/2/pubpaas/US60_NEW_PUB.PEP:
20: /cgm2_6/prodata/2/pubpaas/US60_PUBCOMB.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	617	100.0	116	Sequence 4, Appli
2	516	83.6	535	Sequence 38, Appli
3	511	82.8	112	Sequence 7, Appli
4	507	82.2	136	Sequence 11, Appli
5	507	82.2	136	Sequence 11, Appli
6	507	82.2	136	Sequence 11, Appli
7	507	82.2	136	Sequence 11, Appli
8	507	82.2	136	Sequence 11, Appli
9	507	82.2	136	Sequence 11, Appli
10	507	82.2	136	Sequence 11, Appli
11	507	82.2	136	Sequence 11, Appli
12	507	82.2	136	Sequence 11, Appli
13	507	82.2	136	Sequence 11, Appli

RESULT 1									
; Sequence 4, Application US/10774076									
; Publication No. US20040210040A1									
; GENERAL INFORMATION:									
; APPLICANT: Protein Design Labs, Inc.									
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and									
; FILE REFERENCE: 05882-0064.NPUS01									
; CURRENT APPLICATION NUMBER: US/10-774,076									
; CURRENT FILING DATE: 2004-02-06									
; NUMBER OF SEQ ID NOS: 39									
; SOFTWARE: Patentin version 3.2									
; SEQ ID NO: 4									
; LENGTH: 116									
; TYPE: PRT									
; ORGANISM: mus sp.									
US-10-774-076-4									
Query Match Similarity 100.0%; Score 617; DB 17; Length 116;									
Best Local Similarity 100.0%; Prod. No. 2.2e-48; Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy 1 EVOLQOSGAEVLVRSGASVKL.....YGGTTIPAYWGGTIVTVSA 116									
Db 1 EVOLQOSGAEVLVRSGASVKL.....YGGTTIPAYWGGTIVTVSA 116									
Qy 61 APNFGCRATMADPSNTAVQLQSLTSRDTAVYCYGGTTIPAYWGGTIVTVSA 116									
Db 61 APNFGCRATMADPSNTAVQLQSLTSRDTAVYCYGGTTIPAYWGGTIVTVSA 116									
RESULT 2									
; Sequence 11, Appli									
Sequence 11, Appli									
Sequence 1, Appli									
Sequence 28, Appli									
Sequence 1, Appli									
Sequence 23, Appli									
Sequence 22, Appli									
Sequence 7, Appli									
Sequence 21, Appli									
Sequence 7, Appli									
Sequence 28, Appli									
Sequence 8, Appli									
Sequence 7, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									
Sequence 27, Appli									

Publication No. US20020193561A1

GENERAL INFORMATION:

APPLICANT: CONSELLIER, EMMANUEL
BRACCO, LAURENT

TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL USES THEREOF

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: FINNEGAN, HENDERSON, PARABOW, GARRETT & DUNNER, LLP

STREET: 1300 I Street, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/968,851

FILING DATE: 03-OCT-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/983,035

FILING DATE: 20-Feb-1998

APPLICATION NUMBER: PCT/FR96/01111

FILING DATE: 17-JUL-1996

APPLICATION NUMBER: FR 95/08729

FILING DATE: 19-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Siraus, William L.

REGISTRATION NUMBER: 47,114

REFERENCE/DOCKET NUMBER: 03804.0142

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 535 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 38:

-09-968-851-38

Query Match 83.6%; score 516; DB 9; length 535; Best Local Similarity 84.6%; Pred. No. 8.88-39; Matches 99; Conservative 4; Mismatches 7; Indels 4; Gaps 2; Length: 112; Score: 511; DB 13; Length 112; SEQ ID NO: 11

RESULT 4

US-09-564-329A-11

Sequence 11, Application US/09564329A

Patent No. US20010055751A1

GENERAL INFORMATION:

APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Saffran, Douglas C.

TITLE OF INVENTION: PSA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30135.54US14

CURRENT APPLICATION NUMBER: US/09/564,329A

CURRENT FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: 09/359,326

PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 08/814,279

PRIOR FILING DATE: 1997-03-10

PRIOR APPLICATION NUMBER: 60/071,141

PRIOR FILING DATE: 1998-01-12

PRIOR APPLICATION NUMBER: 60/074,675

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: 60/113,230

PRIOR FILING DATE: 1998-12-21

PRIOR APPLICATION NUMBER: 60/120,536

PRIOR FILING DATE: 1999-02-17

PRIOR APPLICATION NUMBER: 60/124,658

PRIOR FILING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: 09/038,261

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 09/203,939

PRIOR FILING DATE: 1998-12-02

PRIOR APPLICATION NUMBER: 09/251,835

PRIOR FILING DATE: 1999-02-17

PRIOR APPLICATION NUMBER: 09/308,503

PRIOR FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 11

LENGTH: 136

TYPE: PRT

ORGANISM: SCID Mice

US-09-564-329A-11

SUIT 3

10-03-482-7

Sequence 7, Application US/10032482

Publication No. US20020197270A1

GENERAL INFORMATION:

APPLICANT: Cohen, Itum

APPLICANT: ROTTNER, Varla

APPLICANT: Wolkowicz, Roland

APPLICANT: RUIZ, Pedro

APPLICANT: ERIZZ-ALON, Neta

APPLICANT: HERKEL, Johannes

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR TITLE OF INVENTION: IMMUNOTHERAPY

Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

Qy 1 EVOLQSGASLVRSGASVKSCTASGFGNIDKYYIHWVKORPQEGLWIGCIDPENGT 60
Db 14 EVOLQSGASLVRSGASVKSCTASGFGNIDKYYIHWVNQRDQGLEWIGWDPEGT 73

Qy 61 APNFGGRATMADTSNTAYQLQSLSTEDTAVYCYGGTTFAVWQGCTLVSA 116
Db 74 VPKEQKATMADIFSNTAYLHLSSLTSEDTAVYCYKTG---GFWGQGTLTVSA 125

RESULT 5
US-09-853-153-11
; Sequence 11, Application US/09855153
; Patent No. US20020102666A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435_54US14 CURRENT APPLICATION NUMBER: US/09/854,811
CURRENT APPLICATION NUMBER: US/09/855,153 CURRENT FILING DATE: 2001-05-14
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 09/564,329 PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 09/564,329 PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326 PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279 PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141 PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675 PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230 PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536 PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658 PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261 PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939 PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835 PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/318,503 PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 27 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11 LENGTH: 136
TYPE: PRT
ORGANISM: SCID Mice

US-09-854-811-11
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435_54US14 CURRENT APPLICATION NUMBER: US/09/854,811
CURRENT APPLICATION NUMBER: US/09/855,153 CURRENT FILING DATE: 2001-05-14
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 09/564,329 PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 09/564,329 PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326 PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279 PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141 PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675 PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230 PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536 PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658 PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261 PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939 PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/251,835 PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11 LENGTH: 136

RESULT 6
US-09-854-811-11
; Sequence 11, Application US/09854811
; Patent No. US20020119157A1

PRIOR FILING DATE: 1999-07-20 ; SOFTWARE: Patentin Ver. 2.0
; PRIOR APPLICATION NUMBER: 08/814,279 ; SEQ ID NO 11
; PRIOR FILING DATE: 1997-03-10 ; LENGTH: 136
; PRIOR APPLICATION NUMBER: 60/071,141 ;
; PRIOR FILING DATE: 1998-01-12 ; TYPE: PRT
; PRIOR APPLICATION NUMBER: 60/074,675 ; ORGANISM: SCID Mice
; PRIOR FILING DATE: 1998-02-13 ; US-10-224-720-11
; PRIOR APPLICATION NUMBER: 60/113,230 ;
; PRIOR FILING DATE: 1998-12-21 ;
; PRIOR APPLICATION NUMBER: 60/120,536 ;
; PRIOR FILING DATE: 1999-02-17 ;
; PRIOR APPLICATION NUMBER: 60/124,658 ;
; PRIOR FILING DATE: 1999-03-16 ;
; PRIOR APPLICATION NUMBER: 09/038,261 ;
; PRIOR FILING DATE: 1998-03-10 ;
; PRIOR APPLICATION NUMBER: 09/203,939 ;
; PRIOR FILING DATE: 1998-12-02 ;
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-225-784-11;
Query Match 82.2%; Score 507; DB 14; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38; Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
Matches 98;
Qy 1 EVQLOQSGABLVRSGASVKSCTASGFNIDKYYIHWVKORPQEGLWIGCIDPENGDRY 60
Db 14 EVQLOQSGABLVRSGASVKSCTASGFNIDKYYIHWVNQRDQGLEWIGCIDPENGDRP 73
Qy 61 APNFQGRATMTADTSNTAYLQLOSSLTSETDAVYCYGGITFAYWQGQTLVUSA 116
Db 74 VPKFQGKATMTADTSNTAYLHSSLTSDEAVYCKTG---GFWGQGTLVUSA 125
RESULT 11 US-10-225-779-11
; Sequence 11, Application US/10225779
; Publication No. US2003015016A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.5415A
; CURRENT APPLICATION NUMBER: US/10/1225,779
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-225-779-11;
Query Match 82.2%; Score 507; DB 14; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38; Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
Matches 98;
Qy 1 EVQLOQSGABLVRSGASVKSCTASGFNIDKYYIHWVKORPQEGLWIGCIDPENGDRY 60
Db 14 EVQLOQSGABLVRSGASVKSCTASGFNIDKYYIHWVNQRDQGLEWIGCIDPENGDRP 73
Qy 61 APNFQGRATMTADTSNTAYLQLOSSLTSETDAVYCYGGITFAYWQGQTLVUSA 116
Db 74 VPKFQGKATMTADTSNTAYLHSSLTSDEAVYCKTG---GFWGQGTLVUSA 125

RESULT 13 ;
 US-10-374-381-11 ;
 Sequence 11, Application US/10374381 ;
 Publication No. US20030228318A1 ;
 GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 FILE REFERENCE: 30435.54US14
 CURRENT APPLICATION NUMBER: US/10/374,381
 CURRENT FILING DATE: 2003-02-25
 PRIOR APPLICATION NUMBER: US/09/564,329A
 PRIOR FILING DATE: 2000-05-03
 PRIOR APPLICATION NUMBER: 09/359,326
 PRIOR FILING DATE: 1999-07-20
 PRIOR APPLICATION NUMBER: 08/814,279
 PRIOR FILING DATE: 1997-03-10
 PRIOR APPLICATION NUMBER: 60/071,141
 PRIOR FILING DATE: 1998-01-12
 PRIOR APPLICATION NUMBER: 60/074,675
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: 60/113,230
 PRIOR FILING DATE: 1998-12-21
 PRIOR APPLICATION NUMBER: 60/120,536
 PRIOR FILING DATE: 1999-02-17
 PRIOR APPLICATION NUMBER: 60/124,658
 PRIOR FILING DATE: 1999-03-16
 PRIOR APPLICATION NUMBER: 09/038,261
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: 09/203,939
 PRIOR FILING DATE: 1998-12-02
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 11
 LENGTH: 136
 TYPE: PRT
 ORGANISM: SCID Mice
; US-10-374-381-11

Query Match 82.2%; Score 507; DB 14; Length 136;
 Best Local Similarity 84.5%; Pred. No. 2.5e-38; Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
 Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
 QY 1 EVOLQSGASLVRSGASVSKLSTASGENIKDYIHHWKORPEOLEWGCIDPENGTEY 60
 Db 14 EVOLQSGASLVRSGASVSKLSTASGENIKDYIHHWKORPEOLEWGCIDPENGTEY 73
 QY 61 APNFOGRATMDTSSNTAYLQLSLSITSEDAVYCYGGTTFAWGGTIVLVTSA 116
 Db 74 VPKEFQGKATMADFSNTAYLHLSSLTSEDAVYCYCTG---GFWGGTIVLVTSA 125
; US-10-374-381-11

RESULT 14 ;
 US-10-446-542-11 ;
 Sequence 11, Application US/10446542 ;
 Publication No. US20040018571A1 ;
 GENERAL INFORMATION:
 ; APPLICANT: Copley, Clive G
 ; APPLICANT: Edge, Michael Derek
 ; APPLICANT: Emery, Stephen Charles
 ; APPLICANT: Koplowitz, Daniel
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Saffran, Douglas C.
 ; APPLICANT: Witte, Owen N.
 TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
 FILE REFERENCE: 1991-209
 CURRENT APPLICATION NUMBER: US/09/910,059
 CURRENT FILING DATE: 2001-07-23
 PRIOR APPLICATION NUMBER: US 09/171,945
 PRIOR FILING DATE: 1998-10-29
 PRIOR APPLICATION NUMBER: PCT/GB97/01165
 PRIOR FILING DATE: 1997-04-29
 PRIOR APPLICATION NUMBER: GB 9703103.3
 ; PRIOR FILING DATE: 1997-02-14
 ; PRIOR APPLICATION NUMBER: GB9609405.7
 PRIOR FILING DATE: 1996-05-04
 ; NUMBER OF SEQ ID NOS: 131
 SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 11
 LENGTH: 120
 TYPE: PRT
 ORGANISM: Mus musculus
; US-09-910-059-11

Query Match 80.8%; Score 505; DB 9; Length 120;
 Best Local Similarity 80.8%; Pred. No. 3.3e-38;
 Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;
 QY 1 EVOLQSGASLVRSGASVSKLSTASGENIKDYIHHWKORPEOLEWGCIDPENGTEY 60
 Db 1 EVOLQSGASLVRSGASVSKLSTASGENIKDYIHHWKORPEOLEWGCIDPENGTEY 60
; US-09-910-059-11

Mon Jan 3 13:38:52 2005

us-10-774-076-4.rabp

Page 7

QY 61 APNFOGRATMADISSNTAVLQLSSITSEDATVYVC---YGGTITFAWVGQGTIVTVSA 116
|| |; ||: |||: ||||| ||| ||| ||| ||| ||| : ||| ||| ||| |||
Db 61 APKFKOKATIJDASSNTAVLHLSSITSEDATVYCHVLIYAGYLANDYWQGTSVAVSS 120

Search completed: December 29, 2004, 19:41:59
Job time: 69.0678 secs

THIS PAGE BLANK (use reverse)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:37:57 ; Search time 73.5428 Seconds

Scoring table: BLOSUM2 521.928 Million cell updates/sec

Title: US-10-774-076-3

Perfect score: 563

Sequence: 1 DIKMTQSPSSMYASLGERVT.....CLQYDFFPYTFGGGTLKLEIK 107

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_GeneSeq_23Sep04:*

1: genebeqp1980:*

2: genebeqp1990:*

3: genebeqp2000b:*

4: genebeqp2001b:*

5: genebeqp2002a:*

6: genebeqp2003bs:*

7: genebeqp2003bs:*

8: genebeqp2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 556 99.8 107 8 ADE85729 AdE85729 Human Eph

2 556 98.8 107 8 ADL23067 AdL23067 Human Eph

3 554 98.4 237 7 ADE7549 Human Pro

4 554 98.4 237 7 ADD47098 Human Pro

5 554 98.4 237 7 ADD48668 Human Pro

6 551 97.9 355 2 AAW5125 Human R. pipien

7 551 97.9 355 2 AAW5129 R. pipien

8 551 97.9 358 2 AAW5127 R. pipien

9 551 97.9 358 2 AAW5130 R. pipien

10 551 97.9 360 2 AAW35128 R. pipien

11 551 97.9 379 2 AAW5126 R. pipien

12 548 97.3 214 2 AAW27098 Mouse mon

13 546 97.0 127 2 AAR95946 HNK-20 va

14 546 97.0 246 4 AAB86037 Murine an

15 541 96.1 107 2 AAW86050 H65 prote

16 541 96.1 107 8 ADI0167 AdI0167 Murine mo

17 541 96.1 129 2 AAR30880 Aax30880 PXM02. 3/

18 534 94.8 107 6 ABG74702 Murine Mu AbP74702 Murine Mu

19 534 94.8 107 7 ABR3156 AbP83156 Mu007 ant

20 531.5 94.4 215 2 AAR23803 Aax53156 FAB light

21 531 94.3 107 2 AAW23956 Mus muscu

22 529 94.0 105 2 AAW65052 Aaw65052 Human Lc

23 527 93.6 107 2 AAR2083 Aax92083 Murine 13

24 525 93.6 107 5 ABG1430 Aaq31430 Amino aci

25 525 93.3 216 2 AAW15935 Aaw15935 Antibody

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_GeneSeq_23Sep04:*

1: genebeqp1980:*

2: genebeqp1990:*

3: genebeqp2000b:*

4: genebeqp2001b:*

5: genebeqp2002a:*

6: genebeqp2003bs:*

7: genebeqp2003bs:*

8: genebeqp2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 556 99.8 107 8 ADE85729 AdE85729 Human Eph

2 556 98.8 107 8 ADL23067 AdL23067 Human Eph

3 554 98.4 237 7 ADE7549 Human Pro

4 554 98.4 237 7 ADD47098 Human Pro

5 554 98.4 237 7 ADD48668 Human Pro

6 551 97.9 355 2 AAW5125 Human R. pipien

7 551 97.9 355 2 AAW5129 R. pipien

8 551 97.9 358 2 AAW5127 R. pipien

9 551 97.9 358 2 AAW5130 R. pipien

10 551 97.9 360 2 AAW35128 R. pipien

11 551 97.9 379 2 AAW5126 R. pipien

12 548 97.3 214 2 AAW27098 Mouse mon

13 546 97.0 127 2 AAR95946 HNK-20 va

14 546 97.0 246 4 AAB86037 Murine an

15 541 96.1 107 2 AAW86050 H65 prote

16 541 96.1 107 8 ADI0167 AdI0167 Murine mo

17 541 96.1 129 2 AAR30880 Aax30880 PXM02. 3/

18 534 94.8 107 6 ABG74702 Murine Mu

19 534 94.8 107 7 ABR3156 AbP74702 Murine Mu

20 531.5 94.4 215 2 AAR23803 Aax53156 FAB light

21 531 94.3 107 2 AAW23956 Mus muscu

22 529 94.0 105 2 AAW65052 Aaw65052 Human Lc

23 527 93.6 107 2 AAR2083 Aax92083 Murine 13

24 525 93.6 107 5 ABG1430 Aaq31430 Amino aci

25 525 93.3 216 2 AAW15935 Aaw15935 Antibody

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_GeneSeq_23Sep04:*

1: genebeqp1980:*

2: genebeqp1990:*

3: genebeqp2000b:*

4: genebeqp2001b:*

5: genebeqp2002a:*

6: genebeqp2003bs:*

7: genebeqp2003bs:*

8: genebeqp2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 556 99.8 107 8 ADE85729 AdE85729 Human Eph

2 556 98.8 107 8 ADL23067 AdL23067 Human Eph

3 554 98.4 237 7 ADE7549 Human Pro

4 554 98.4 237 7 ADD47098 Human Pro

5 554 98.4 237 7 ADD48668 Human Pro

6 551 97.9 355 2 AAW5125 Human R. pipien

7 551 97.9 355 2 AAW5129 R. pipien

8 551 97.9 358 2 AAW5127 R. pipien

9 551 97.9 358 2 AAW5130 R. pipien

10 551 97.9 360 2 AAW35128 R. pipien

11 551 97.9 379 2 AAW5126 R. pipien

12 548 97.3 214 2 AAW27098 Mouse mon

13 546 97.0 127 2 AAR95946 HNK-20 va

14 546 97.0 246 4 AAB86037 Murine an

15 541 96.1 107 2 AAW86050 H65 prote

16 541 96.1 107 8 ADI0167 AdI0167 Murine mo

17 541 96.1 129 2 AAR30880 Aax30880 PXM02. 3/

18 534 94.8 107 6 ABG74702 Murine Mu

19 534 94.8 107 7 ABR3156 AbP74702 Murine Mu

20 531.5 94.4 215 2 AAR23803 Aax53156 FAB light

21 531 94.3 107 2 AAW23956 Mus muscu

22 529 94.0 105 2 AAW65052 Aaw65052 Human Lc

23 527 93.6 107 2 AAR2083 Aax92083 Murine 13

24 525 93.6 107 5 ABG1430 Aaq31430 Amino aci

25 525 93.3 216 2 AAW15935 Aaw15935 Antibody

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_GeneSeq_23Sep04:*

1: genebeqp1980:*

2: genebeqp1990:*

3: genebeqp2000b:*

4: genebeqp2001b:*

5: genebeqp2002a:*

6: genebeqp2003bs:*

7: genebeqp2003bs:*

8: genebeqp2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 556 99.8 107 8 ADE85729 AdE85729 Human Eph

2 556 98.8 107 8 ADL23067 AdL23067 Human Eph

3 554 98.4 237 7 ADE7549 Human Pro

4 554 98.4 237 7 ADD47098 Human Pro

5 554 98.4 237 7 ADD48668 Human Pro

6 551 97.9 355 2 AAW5125 Human R. pipien

7 551 97.9 355 2 AAW5129 R. pipien

8 551 97.9 358 2 AAW5127 R. pipien

9 551 97.9 358 2 AAW5130 R. pipien

10 551 97.9 360 2 AAW35128 R. pipien

11 551 97.9 379 2 AAW5126 R. pipien

12 548 97.3 214 2 AAW27098 Mouse mon

13 546 97.0 127 2 AAR95946 HNK-20 va

14 546 97.0 246 4 AAB86037 Murine an

15 541 96.1 107 2 AAW86050 H65 prote

16 541 96.1 107 8 ADI0167 AdI0167 Murine mo

17 541 96.1 129 2 AAR30880 Aax30880 PXM02. 3/

18 534 94.8 107 6 ABG74702 Murine Mu

19 534 94.8 107 7 ABR3156 AbP74702 Murine Mu

20 531.5 94.4 215 2 AAR23803 Aax53156 FAB light

21 531 94.3 107 2 AAW23956 Mus muscu

22 529 94.0 105 2 AAW65052 Aaw65052 Human Lc

23 527 93.6 107 2 AAR2083 Aax92083 Murine 13

24 525 93.6 107 5 ABG1430 Aaq31430 Amino aci

25 525 93.3 216 2 AAW15935 Aaw15935 Antibody

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_GeneSeq_23Sep04:*

1: genebeqp1980:*

2: genebeqp1990:*

3: genebeqp2000b:*

4: genebeqp2001b:*

5: genebeqp2002a:*

6: genebeqp2003bs:*

7: genebeqp2003bs:*

8: genebeqp2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 556 99.8 107 8 ADE85729 AdE85729 Human Eph

2 556 98.8 107 8 ADL23067 AdL23067 Human Eph

3 554 98.4 237 7 ADE7549 Human Pro

4 554 98.4 237 7 ADD47098 Human Pro

5 554 98.4 237 7 ADD48668 Human Pro

6 551 97.9 355 2 AAW5125 Human R. pipien

7 551 97.9 355 2 AAW5129 R. pipien

8 551 97.9 358 2 AAW5127 R. pipien

9 551 97.9 358 2 AAW5130 R. pipien

10 551 97.9 360 2 AAW35128 R. pipien

11 551 97.9 379 2 AAW5126 R. pipien

12 548 97.3 214 2 AAW27098 Mouse mon

13 546 97.0 127 2 AAR95946 HNK-20 va

14 546 97.0 246 4 AAB86037 Murine an

CC antibody that binds EphA2 with a K_{off} of less than 3 × 10⁻³ s⁻¹. Also
 CC described: (1) a pharmaceutical composition comprising a therapeutic
 CC amount of (1) and a pharmaceutical carrier; (2) a cell line that produces
 CC (I); (3) a hybridoma deposited with the ATCC accession number PTA-4572,
 CC PTA-4573 or PTA-4574; (4) an isolated nucleic acid comprising a
 CC nucleotide sequence encoding a light chain variable domain or a heavy
 CC chain variable domain of the EphA2 antibody; (5) a vector comprising the
 CC nucleic acid described above; (6) a host cell comprising the vector; (7)
 CC methods of identifying the EphA2 agonistic antibody or the EphA2 antibody
 CC that inhibits a cancer cell phenotype, that kills cancer cells having a
 CC cancer cell phenotype or that preferentially binds an EphA2 epitope
 CC exposed on cancer cells; and (8) a method of diagnosing, prognosis or
 CC monitoring the efficacy of therapy for cancer in a patient known to or
 CC suspected to have cancer. (I) has cyrostatic, anti-psoriatic,
 CC antipsoriatric, anti-inflammatory, vasoconstrictive and respiratory activities,
 CC and can be used in gene therapy. The composition and methods are useful
 CC in managing, diagnosing, preventing or treating hyperproliferative cell
 CC diseases (i.e. metastatic cancer) or non-cancer hyperproliferative cell
 CC disease, smooth muscle restenosis, endothelial restenosis, Crohn's
 CC disease, or chronic obstructive pulmonary disease. They may also be used
 CC for monitoring the efficacy of therapy for cancer in a patient known to
 CC or suspected to have cancer, and in screening for anti-cancer drugs. The
 CC present sequence is used in the exemplification of the present invention.

SQ Sequence 107 AA;

Query Match 98.8%; Score 556; DB 8; Length 107;
 Best Local Similarity 98.1%; Pred. No. 5e-37; 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIKMTQSPSMSWASLGERVTICKAKASODINNLYSLWFOQKGSKPTKLIVANRLVDGVPs 60
 Db 1 DIKMTQSPSMSWASLGERVTICKAKASODINNLYSLWFOQKGSKPTKLIVANRLVDGVPs 60

QY 61 RPSGSGSGQDYLTSLEVEDMGIVYCLQDEFYTRGGTKEIK 107
 Db 61 RPSGSGSGQDYLTSLEVEDMGIVYCLQDEFYTRGGTKEIK 107

RESULT 2

ID ADL23067 ID ADL23067 standard; protein; 107 AA.

AC ADL23067;

DT 20-MAY-2004 (first entry)

DE Human EphA2 antibody VL chain.

KW antibody; human; EphA2; variable light chain; VL chain; cancer;
 KW cytostatic.

OS Homo sapiens.

XX WO2004014292-A2.

XX 19-FEB-2004.

PP 12-MAY-2003; 2003WO-US015046.

PR 10-MAY-2002; 2002US-0379368P.
 PR 14-OCT-2002; 2002US-0418204P.
 PR 03-APR-2003; 2003US-0460358P.

PA (PURD) PURDUE RES FOUND.

PT Kinch MS, Carles-Kinch K;

XX WPI; 2004-180531-17.

DR N-PSDB; ADL23075.

XX PT Treating cancer, e.g. breast, lung, prostate, or skin cancer, comprises

PT administering an EphA2 antibody that is an EphA2 agonistic antibody or an
 PT exposed EphA2 epitope antibody.

PT XX Claim 49; FIG 16A; 124pp; English.

CC The present invention relates to a method of treating cancer (fully or
 CC partially refractory to a first treatment), comprising administering an
 CC EphA2 antibody, that is an EphA2 agonistic antibody or an exposed EphA2
 CC epitope antibody. The method is useful for treating, managing or
 CC preventing cancer (e.g. lung, colon, prostate, breast or skin cancer),
 CC particularly metastatic cancer. The method may be used not only in
 CC unresected patients but also in the treatment of patients partially or
 CC refractory to current standard and experimental cancer therapies, e.g.
 CC chemotherapies or hormonal therapies, to improve the efficacy of such
 CC treatments. The present sequence is the human EphA2 antibody VL chain.

SQ Sequence 107 AA;

Query Match 98.8%; Score 556; DB 8; Length 107;
 Best Local Similarity 98.1%; Pred. No. 5e-37; 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIKMTQSPSMSWASLGERVTICKAKASODINNLYSLWFOQKGSKPTKLIVANRLVDGVPs 60
 Db 1 DIKMTQSPSMSWASLGERVTICKAKASODINNLYSLWFOQKGSKPTKLIVANRLVDGVPs 60

QY 61 RPSGSGSGQDYLTSLEVEDMGIVYCLQDEFYTRGGTKEIK 107
 Db 61 RPSGSGSGQDYLTSLEVEDMGIVYCLQDEFYTRGGTKEIK 107

RESULT 3
 DE ID ADE57549 standard; protein; 237 AA.

AC ADE57549;
 XX DR 29-JAN-2004 (first entry)

DE Human Protein S65921, SEQ ID NO 3411.

XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 XX spared nerve injury; SNI; Chung.

OS Homo sapiens.

XX WO2003016475-A2.

XX PD 27-FEB-2003.

XX PP 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX PI Woolf C, Durso D, Befort K, Costigan M;

XX WPI; 2003-268312-26.

DR GENBANK; S65921.

XX PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 101pp; English.

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also

claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp wipo.int/pub/published_pct_sequences.

Sequence 237 AA;

Query Match 98.4%; Score 554; DB 7; Length 237;
Best Local Similarity 99.1%; Pred. No. 1.6e-36;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASIGERVTITCKASQDINSYLSWFOQQPKGSKPPTLYRANLVDGVPS 60
23 DIKMTQSPSSMYASIGERVTITCKASQDINSYLSWFOQQPKGSKPPTLYRANLVDGVPS 82
QY 61 RFSGSGSGQYSLTISLEYEDMGIVYCYQDYEPRTFEGGTKLRIK 107
83 RFSGSGSGQYSLTISLEYEDMGIVYCYQDYEPRTFEGGTKLRIK 129

Db RESULT 4

ADD7098 ADD7098 standard; protein; 237 AA.
AC ADD7098;
XX DT 29-JAN-2004 (first entry)

XX Human Protein S65921, SEQ ID NO 12786.
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.

XX Homo sapiens.
XX WO2003016475-A2.
XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;
DR WPI; 2003-268312/26.

Sequence 237 AA;

Query Match 98.4%; Score 554; DB 7; Length 237;
Best Local Similarity 99.1%; Pred. No. 1.6e-36;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASIGERVTITCKASQDINSYLSWFOQQPKGSKPPTLYRANLVDGVPS 60
23 DIKMTQSPSSMYASIGERVTITCKASQDINSYLSWFOQQPKGSKPPTLYRANLVDGVPS 82
QY 61 RFSGSGSGQYSLTISLEYEDMGIVYCYQDYEPRTFEGGTKLRIK 107
83 RFSGSGSGQYSLTISLEYEDMGIVYCYQDYEPRTFEGGTKLRIK 129

Db RESULT 5

ADD48668 ADD48668 standard; protein; 237 AA.
AC ADD48668;
XX DT 29-JAN-2004 (first entry)

XX Human Protein S65921, SEQ ID NO 14374.

XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0346382P.
PR 01-NOV-2001; 2001US-0312147P.

XX New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polypeptides given in the specification, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp wipo.int/pub/published_pct_sequences.

XX Sequence 237 AA;

Query Match 98.4%; Score 554; DB 7; Length 237;
Best Local Similarity 99.1%; Pred. No. 1.6e-36;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASIGERVTITCKASQDINSYLSWFOQQPKGSKPPTLYRANLVDGVPS 60
23 DIKMTQSPSSMYASIGERVTITCKASQDINSYLSWFOQQPKGSKPPTLYRANLVDGVPS 82
QY 61 RFSGSGSGQYSLTISLEYEDMGIVYCYQDYEPRTFEGGTKLRIK 107
83 RFSGSGSGQYSLTISLEYEDMGIVYCYQDYEPRTFEGGTKLRIK 129

Db RESULT 4

ADD7098 ADD7098 standard; protein; 237 AA.
AC ADD7098;
XX DT 29-JAN-2004 (first entry)

XX Human Protein S65921, SEQ ID NO 12786.
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GENO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

DR WPI; 2003-268312/26.

XX GENBANK; S65921.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PT Rybak SM, Newton DL, Boque L, Wlodawer A;
 XX
 DR WPI; 1997-435168/40.
 DR N-PSDB; AT94967.
 PT Ribonuclease molecules based on native Onconase - used for killing cells,
 particularly tumour cells.
 XX Disclosure; Page 71; 90pp; English.

PS Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
 (rOnC) which are modifications of the RNase Onconase (RTm) (nOnC). Such
 novel ribonuclease molecules are highly cytotoxic and can be used alone
 or to form chemical conjugates or to target recombinant immunofusions.
 CC They are used particularly for decreasing tumour cell growth. They can
 also be used for cell separation in vitro by selectively killing unwanted
 types of cells, e.g. in bone marrow prior to transplantation into a
 patient undergoing marrow ablation by radiation, or for killing leukaemia
 cells or T-cells that would cause graft versus host disease. The toxins
 can also be used to selectively kill unwanted cells in culture. The new
 ribonucleases have increased cytotoxic activity compared to nOnC and also
 lower immunogenicity in humans

CC Sequence 358 AA;

Query Match 97.9%; Score 551; DB 2; Length 355;
 Best Local Similarity 97.2%; Pred. No. 4e-36; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 104; Conservative 1; MisMatch 0;

QY 1 DIKMTQSPSSMVASLGERVTICKASQDINSYLSWFOQKPGKSPKLTYRANRLVDGVPS 60
 Db 1 DIKMTQSPSSMVASLGERVTICKASQDINSYLSWFOQKPGKSPKLTYRANRLVDGVPS 60

QY 61 RFSSGGSGDYSLTSLEYEDMGIVYCLQYDERPYTFCGGTKLIK 107
 Db 61 RFSSGGSGDYSLTSLEYEDMGIVYCLQYDERPYTFCGGTKLIK 107

Db 61 RFSSGGSGDYSLTSLEYEDMGIVYCLQYDERPYTFCGGTKLIK 107

RESULT 8
 AAW35127 ID AAW35127 Standard; protein; 358 AA.
 XX
 AC AAM35127;
 XX
 DT 20-APR-1998 (first entry)

R. pipiens recombinant RNase rOnC fusion protein 3.

KW RNase A; ribonuclease; cytotoxic; onconase; nOnC; immunofusion;
 KW tumour cell growth; frog.
 OS Rana Pipiens.
 OS Synthetic.

XX
 PN WO9731116-A2.

XX
 PD 28-AUG-1997.

XX
 PR 19-FEB-1997; 97WO-US002588.

XX
 PR 21-FEB-1996; 96US-0011800P.

XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Rybak SM, Newton DL, Boque L, Wlodawer A;

XX
 DR WPI; 1997-435168/40.
 DR N-PSDB; AT94968.

PT Ribonuclease molecules based on native Onconase - used for killing cells,
 particularly tumour cells.

XX Disclosure; Page 72; 90pp; English.

XX
 CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
 (rOnC) which are modifications of the RNase Onconase (RTm) (nOnC). Such
 novel ribonuclease molecules are highly cytotoxic and can be used alone
 or to form chemical conjugates or to target recombinant immunofusions.
 CC They are used particularly for decreasing tumour cell growth. They can
 also be used for cell separation in vitro by selectively killing unwanted

CC cells or T-cell that would cause graft versus host disease. The toxins
 can also be used to Selectively kill unwanted cells in culture. The new
 ribonucleases have increased cytotoxic activity compared to nOnC and also
 lower immunogenicity in humans

XX Sequence 358 AA;

Query Match 97.9%; Score 551; DB 2; Length 358;
 Best Local Similarity 97.2%; Pred. No. 4e-36; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 104; Conservative 1; MisMatch 0;

QY 1 DIKMTQSPSSMVASLGERVTICKASQDINSYLSWFOQKPGKSPKLTYRANRLVDGVPS 60
 Db 1 DIKMTQSPSSMVASLGERVTICKASQDINSYLSWFOQKPGKSPKLTYRANRLVDGVPS 60

QY 119 DIKMTQSPSSMVASLGERVTICKASQDINSYLSWFOQKPGKSPKLTYRANRLVDGVPS 178
 Db 119 DIKMTQSPSSMVASLGERVTICKASQDINSYLSWFOQKPGKSPKLTYRANRLVDGVPS 178

RESULT 9
 AAW35130 ID AAW35130 Standard; protein; 358 AA.
 XX
 AC AAM35130;
 XX
 DT 20-APR-1998 (first entry)

R. pipiens recombinant RNase rOnC fusion protein 6.

KW RNase A; ribonuclease; cytotoxic; onconase; nOnC; immunofusion;
 KW tumour cell growth; frog.
 OS Rana pipiens.
 OS Synthetic.

XX
 PN WO9731116-A2.

XX
 PD 28-AUG-1997.

XX
 PR 19-FEB-1997; 97WO-US002588.

XX
 PR 21-FEB-1996; 96US-0011800P.

XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Rybak SM, Newton DL, Boque L, Wlodawer A;

XX
 DR WPI; 1997-435168/40.
 DR N-PSDB; AT94968.

PT Ribonuclease molecules based on native Onconase - used for killing cells,
 particularly tumour cells.

XX Disclosure; Page 72; 90pp; English.

XX
 CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
 (rOnC) which are modifications of the RNase Onconase (RTm) (nOnC). Such
 novel ribonuclease molecules are highly cytotoxic and can be used alone
 or to form chemical conjugates or to target recombinant immunofusions.
 CC They are used particularly for decreasing tumour cell growth. They can
 also be used for cell separation in vitro by selectively killing unwanted

CC types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins CC can also be used to selectively kill unwanted cells in culture. The new CC ribonucleases have increased cytotoxic activity compared to nOnc and also lower immunogenicity in humans.

XX Sequence 358 AA;

Query Match 97.9%; Score 551; DB 2; Length 358;
Best Local Similarity 97.2%; Pred. No. 4 1e-36;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIKMTQSSSMYLGERVTICKASODINNSLWSFOOKPGSKSPKTLYRANRLVGVPS 60
Db 119 DIKMTQSSSMYLGERVTICKASODINNSLWSFOOKPGSKSPKTLYRANRLVGVPS 178

QY 61 RFSGSGGSDQDYSITISLEVEYEDMGIVYCLQDEFPYTFGSGTKEIK 107
Db 179 RFSGSGGSDQDYSITISLEVEYEDMGIVYCLQDEFPYTFGSGTKEIK 225

RESULT 10
AAW35128

ID AAW35128 standard; protein; 360 AA.
XX
AC AAW35128;
DT 20-APR-1998 (first entry)

DE R. pipiens recombinant RNase rOnc fusion protein 4.
RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW tumour cell growth; frog.
XX
OS Rana pipiens.
OS Synthetic.
XX
PN W09731116-A2.
XX
PD 28-AUG-1997.
XX
PR 19-FEB-1997; 97WO-US002588.
XX
PR 19-FEB-1997; 97WO-US002588.
XX
PR 21-FEB-1997; 96US-0011800P.
XX
PR 21-FEB-1997; 96US-0011800P.
XX
DR WPI; 1997-435168/40.
XX
N-PSDB; AT94964.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL, Boque L, Wlodawer A;
XX
DR WPI; 1997-435168/40.
XX
PT Ribonuclease molecules based on native Onconase - used for killing cells,
XX
PS Disclosure; Page 6B; 90pp; English.

XX
sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC (rOnc) which are modifications of the RNase Onconase (rOnc). Such
CC novel ribonuclease molecules are highly cytotoxic and can be used alone
or to form chemical conjugates or to target recombinant immunofusions.
CC They are used particularly for decreasing tumour cell growth. They can
CC also be used for cell separation in vitro by selectively killing unwanted
CC types of cells, e.g. in bone marrow prior to transplantation into a
CC patient undergoing marrow ablation by radiation, or for killing leukaemia
CC cells or T-cells that would cause graft versus host disease. The toxins
CC can also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nOnc and also
CC lower immunogenicity in humans.

XX Sequence 379 AA;

Query Match 97.9%; Score 551; DB 2; Length 360;
Best Local Similarity 97.2%; Pred. No. 4 1e-36;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIKMTQSSSMYLGERVTICKASODINNSLWSFOOKPGSKSPKTLYRANRLVGVPS 60
Db 121 DIKMTQSSSMYLGERVTICKASODINNSLWSFOOKPGSKSPKTLYRANRLVGVPS 180

QY 61 RFSGSGGSDQDYSITISLEVEYEDMGIVYCLQDEFPYTFGSGTKEIK 107
Db 181 RFSGSGGSDQDYSITISLEVEYEDMGIVYCLQDEFPYTFGSGTKEIK 227

RESULT 11
AAW35126

ID AAW35126 standard; protein; 379 AA.
XX
AC AAW35126;
DT 20-APR-1998 (first entry)

DE R. pipiens recombinant RNase rOnc fusion protein 2.
RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW tumour cell growth; frog.
XX
OS Rana pipiens.
OS Synthetic.
XX
PN W09731116-A2.
XX
PD 28-AUG-1997.
XX
PR 19-FEB-1997; 97WO-US002588.
XX
PR 21-FEB-1997; 96US-0011800P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL, Boque L, Wlodawer A;
XX
DR WPI; 1997-435168/40.
XX
N-PSDB; AT94964.

PT Ribonuclease molecules based on native Onconase - used for killing cells,
XX
PS Disclosure; Page 6B; 90pp; English.

XX
sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC (rOnc) which are modifications of the RNase Onconase (rOnc). Such
CC novel ribonuclease molecules are highly cytotoxic and can be used alone
or to form chemical conjugates or to target recombinant immunofusions.
CC They are used particularly for decreasing tumour cell growth. They can
CC also be used for cell separation in vitro by selectively killing unwanted
CC types of cells, e.g. in bone marrow prior to transplantation into a
CC patient undergoing marrow ablation by radiation, or for killing leukaemia
CC cells or T-cells that would cause graft versus host disease. The toxins
CC can also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nOnc and also
CC lower immunogenicity in humans.

XX Sequence 379 AA;

Query Match 97.9%; Score 551; DB 2; Length 379;
Best Local Similarity 97.2%; Pred. No. 4 3e-36;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIKMTQSSSMYLGERVTICKASODINNSLWSFOOKPGSKSPKTLYRANRLVGVPS 60
Db 143 DIKMTQSSSMYLGERVTICKASODINNSLWSFOOKPGSKSPKTLYRANRLVGVPS 202

QY 61 RFSGSGGSDQDYSITISLEVEYEDMGIVYCLQDEFPYTFGSGTKEIK 107
Db 143 DIKMTQSSSMYLGERVTICKASODINNSLWSFOOKPGSKSPKTLYRANRLVGVPS 202

Sequence 360 AA;

Db 203 RFSGSGSGQDYSLTISLEYDMGIYCYLQYDEFPYTFGGTKLEIK 249
 RESULT 12
 AAW27089 standard; protein; 214 AA.
 XX
 ID AAW27089;
 AC XX
 DT 18-NOV-1997 (first entry)
 XX
 DB Mouse monoclonal antibody B9 light chain.
 XX
 KW Human plasma apolipoprotein B-100; arteriosclerotic lipoprotein;
 KW antibody; Fab.
 XX
 OS Mus musculus.
 XX
 FH Location/Qualifiers
 Key 24-.34
 Region /label= CDR1
 FT 50-.56
 Region /label= CDR2
 FT 89-.97
 Region /label= CDR3
 FT 108-.214
 PT /label= Ckappa
 XX
 JP09154587-A.
 XX
 PD 17-JUN-1997.
 XX
 PR 09-MAY-1996; 96JP-00114492.
 PR 02-NOV-1995; 95KR-00039459.
 PR (KOAD) KOREAN SCI & TECHNOLOGY RES CENT.
 XX
 DR WPI; 1997-367067/34.
 DR N-PSDB; NAT85091.
 XX
 PA DNA encoding mouse antibody binding human plasma apo-lipoprotein B-100 -
 XX useful for removing arteriosclerotic lipoprotein(s).
 DR
 PS Claim 4; Fig 6; 17pp; Japanese.
 XX
 PT The present sequence represents the mouse monoclonal antibody B9 light
 XX chain (B9L), which binds specifically to human blood apolipoprotein B-
 XX 100. The nucleic acid can be used in a method for the preparation of a
 CC reconstituted antibody which specifically binds human plasma
 CC apolipoprotein B-100. The antibody can be used as a reagent for
 CC determining the concentration of human plasma apolipoprotein B-100 in a
 CC drug composition for selectively removing arteriosclerotic lipoproteins containing human plasma
 CC apolipoprotein B-100
 XX
 SQ Sequence 214 AA;
 Query Match 97.3%; Score 548; DB 2; Length 214;
 Best Local Similarity 97.2%; Pred. No. 4.3e-36; Indels 0; Gaps 0;
 Matches 104; Conservative 2; Mismatches 1;
 Qy 1 DIKMQQSPSSMMASIGERVTICKASODINNSYLSWFOOKPKGSKPPLIYRANRLVDPVS 60
 Db 1 DIKMQQSPSSMMASIGERVTICKASODINNSYLSWFOOKPKGSKPPLIYRANRLVDPVS 60
 61 RPSSGGSGQDYSLTISLEYDMGIYCYLQYDEFPYTFGGTKLEIK 107
 Qy 61 RPSSGGSGQDYSLTISLEYDMGIYCYLQYDEFPYTFGGTKLEIK 107
 Db 81 RPSSGGSGQDYSLTISLEYDMGIYCYLQYDEFPYTFGGTKLEIK 127

AAR95946 ID AAR95946 standard; protein; 127 AA.
 XX
 AC AAR95946;
 DT 10-FEB-1997 (first entry)
 XX
 DB HNK-20 variable kappa chain.
 XX
 KW Antibody; HNK-20; variable kappa chain; hybridoma; murine; IgA; mouse;
 KW F glycoprotein; respiratory syncytial virus; RSV; constant region gene;
 KW chimeric antibody; isotype-switched antibody; therapy; infection; human;
 KW pneumonia; bronchiolitis; animal.
 XX
 OS Mus musculus.
 XX
 PN W09616974-A1.
 XX
 PD 06-JUN-1996.
 XX
 PR 01-DEC-1995; 95MO-US015715.
 XX
 PR 01-DEC-1994; 94US-00348548.
 XX
 PA (ORAV-) ORAVAX INC.
 XX
 PI Berdoz J, Kraehenbuhl J;
 XX
 DR WPI; 1996-286826/29.
 DR N-PSDB; AAT30455.
 XX
 PT DNA encoding variable region of antibody HNK-20 - for treating
 XX respiratory syncytial virus infection.
 XX
 PS Claim 9; Page 30; 75pp; English.
 XX
 CC AAR95946-R95948 represent sequences for variable regions of an antibody
 CC produced by the hybridoma cell line HNK-20. This sequence represents the
 CC sequence for the antibody HNK-20 variable kappa chain. HNK-20 is a murine
 CC hybridoma cell line, that produces IgA specific for the F glycoprotein of
 CC respiratory syncytial virus (RSV). The DNA encoding these sequences were
 CC isolated using primers specific for the 5' untranslated region of the
 CC variable region, and for the intron downstream of the rearranged J region
 CC (see AAT30455-T30545 for primer sequences). The DNA encoding these
 CC sequences can be inserted into vectors containing heterologous (such as
 CC human) constant region genes, for the production of chimeric and isotype-
 CC switched antibodies. The antibodies are useful in the treatment and
 CC diagnosis of infection by RSV, such as pneumonia and bronchiolitis, in
 CC humans and animals. By using genomic DNA as a template, variable region
 CC genes can be isolated without producing fragments that have to be adapted
 CC for recombinant antibody expression. Also, by using the genomic DNA, no
 CC knowledge of the DNA sequence encoding the target variable region is
 CC required. Chimeric antibodies produced from these proteins, that contain
 CC the constant region of the host being treated, are less likely to cause
 CC adverse immune reactions
 XX
 SQ Sequence 127 AA;
 Query Match 97.0%; Score 546; DB 2; Length 127;
 Best Local Similarity 95.3%; Pred. No. 3.7e-36; Indels 0; Gaps 0;
 Matches 102; Conservative 5; Mismatches 0;
 Qy 1 DIKMQQSPSSMMASIGERVTICKASODINNSYLSWFOOKPKGSKPPLIYRANRLVDPVS 60
 Db 21 DIKMQQSPSSMMASIGERVTICKASODINNSYLSWFOOKPKGSKPPLIYRANRLVDPVS 80
 61 RPSSGGSGQDYSLTISLEYDMGIYCYLQYDEFPYTFGGTKLEIK 107
 Qy 61 RPSSGGSGQDYSLTISLEYDMGIYCYLQYDEFPYTFGGTKLEIK 107
 Db 81 RPSSGGSGQDYSLTISLEYDMGIYCYLQYDEFPYTFGGTKLEIK 127

ID AAB86037 standard; protein; 246 AA.
 XX
 AC AAB86037;
 XX DT 16-JUL-2001 (first entry)
 XX DE Murine anti-CA19-9 antigen protein.
 XX KW Antigen; CA19-9; murine; variable heavy chain; VH; anti-CA19-9; cancer; variable light chain; VL; cytostatic; detection; stomach tumor cell; pancreas tumor cell; immunotherapy; single-chain Fv; drug targeting; KW prodrug activation.
 XX OS Mus sp.
 OS Synthetic.
 XX FH Key
 FT Domain Location/Qualifiers
 FT Region 5..113
 /label= VH
 114..144
 /note= "Linker segment"
 FT Domain 145..244
 /label= VL
 PN EP1090927-A1.
 XX PD 11-APR-2001.
 XX PP 08-OCT-1999; 99EP-00120119.
 PR 08-OCT-1999; 99EP-00120119.
 XX PA (ABKE/) ABKEN H.
 XX PI Abken H;
 XX DR WPI; 2001-345810/37.
 DR N-PSDB; AAF88024.
 XX PT New single-chain Fv fragment specific for antigen CA19-9, useful for diagnosis and treatment of tumors, particularly of stomach and pancreas.
 XX PS Claim 6; Fig 1; 23pp; German.

This invention describes a novel polypeptide {I}, comprising an oligopeptide (Op1) having the variable region of the heavy chain (VH) of an anti-CA19-9 antibody (Ab), or its fragment with the same binding specificity for CA19-9 antigen, and an oligopeptide (Op2) based on the variable light chain (VL) region of an Ab, or its fragment, is new. Op1 and Op2 are linked directly or through a linker peptide (Lp). The products of the invention have cytostatic activity. {I}, optionally in radiolabeled form or fused to other active substances, is used as pharmaceutical or diagnostic agent for detection, localization and/or elimination of cells that express the CA19-9 antigen, especially stomach or pancreas tumor cells. When linked to other binding domains, {I} can be used to produce bi- or multi-specific antibodies, also useful for immunotherapy of cancers. {I}, a single-chain Fv fragment has good solubility in water, is renaud to active form very efficiently after denaturation, penetrates tissue well, and accumulates on CA19-9 presenting cells *in vivo*, but not on normal cells. {I} is not internalized by the cells, and has a long residence time on the cell surface, without degradation by cytoplasmic proteases, making it well suited for drug targeting, or prodrug activation. Since {I} do not include murine constant regions, it should be possible to administer them repeatedly without inducing a human anti-murine antibody response. Also, when coupled to the human CH2CH3 immunoglobulin domains, they cause specific lysis of tumor cells. This sequence represents the mouse derived anti-CA19-9 antibody construct described in the method of the invention

Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 DIKMQSPSSMSWYASIGERTVICKASQDINSLSWRQPKGSKPQKTLIYRANLIVGVPs 60
 Db 137 DIQMQSPSSMSWYASIGERTVICKASQDINSLSWRQPKGSKPQKTLIYRANLIVGVPs 196
 Qy 61 RFSGSGSCDYSLTISLEYEDMGIVYCLQIDEPFPYTFGGGTLEIK 107
 Db 197 RFSGGGSCDYSLTISLEYEDMGIVYCLQYDEPRFGGCKLEIK 243

RESULT 15

AAM58505
 ID AAM58505 standard; protein; 107 AA.
 XX AC AAM58505;
 XX DT 18-AUG-1998 (first entry)

H65 protein sequence SEQ ID NO:26 from FIG 6.
 XX KW Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin; depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis; autoimmune disease; rheumatoid arthritis; type I diabetes.

Mus sp.
 XX US5770196-A.

XX PD 23-JUN-1998.

XX PR 07-JUN-1995; 95US-00472788.

XX PR 13-DEC-1991; 91US-00808464.

XX PR 14-DEC-1992; 92WO-US010906.

XX PR 23-JUN-1993; 93US-00082842.

XX DR (XOMA) XOMA CORP.

XX PA Studnicka GM;

XX PS WPI; 1998-376744/32.

Depletion of CD5-positive cells *in vivo* - using anti-CD5 antibodies with humanised variable regions.

Example 6; Col 61-64; 77pp; English.

A method has been developed of depleting CD5+ cells *in vivo*. The method comprises administering a cytotoxic protein containing a modified immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig molecule or an immunoconjugate or fusion protein containing an anti-CD5 Ig molecule, and where the modified Ig variable domain comprises at least one of (a) a modified light chain variable region (see AAM5478 or AAM8480), and (b) a modified heavy chain variable region (see AAM58479 or AAM58481), where AAM58479 and AAM5849 are humanised forms of the H65 light and heavy chain variable domains with low risk amino acid substitutions [i.e. low risk of reducing antigen-binding specificity]. CC AAM58480 and AAM58481 are humanised forms of the H65 light and heavy chain variable domains with moderate risk amino acid substitutions and are present in humanised H65 antibody he3 (ARCC HB 11206). The method is useful for treating autoimmune diseases, especially systemic lupus erythematosus, rheumatoid arthritis, psoriasis or type I diabetes. The present sequence represents an H65 sequence from the present invention

Sequence 107 AA;

Query Match 96.1%; Score 541; DB 2; length 107;

Best Local Similarity 96.3%; Pred. No. 7..9e-36;

Best Local Similarity 97.2%; Pred. No. 7e-36;

Length 246;

SQ Sequence 246 AA;

Query Match 97.0%; Score 546; DB 4;

Length 246;

Best Local Similarity 97.2%; Pred. No. 7e-36;

Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIKMQSPSSMSWYASIGERTVICKASQDINSLSWRQPKGSKPQKTLIYRANLIVGVPs 60

Mon Jan 3 13:38:50 2005

Db 1 DIKMTQSPSSMYASILGRVITCKASQDINSYLSWQQKGKSPKTLIVANRLVDGVPS 60
Qy 61 RFSGSGSGOYSLTISLEEDMGIYCYCQYDEFPTFGGTKLBIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGSGOYSLTISLDEDMGIYCYCQYDESPWTFGGTKLBIK 107

Search completed: December 29, 2004, 17:57:26
Job time : 76.5428 secs

THIS PAGE IS A LIE
(1979)

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] DR HSSP; P80362; IgM.
 RP DR InterPro; IPR00110; Ig-like.
 CC DR InterPro; IPR003596; Ig_v.
 RA DR SMART; SM00407; Ig; 1.
 DR DR PROSITE; PS50835; IgV; 1.
 RL DR IMMUNOGLOBULIN V REGION; Signal.
 DR DR GO; GO:0005634; C:nucleus; IEA.
 DR DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR DR InterPro; IPR001356; Homeobox.
 DR DR InterPro; IPR007110; Ig-like.
 DR DR InterPro; IPR003597; Ig cl.
 DR DR InterPro; IPR00306; Ig MHC.
 DR DR Pfam; PF07654; Cl-set; T.
 DR DR Pfam; PF00047; Ig; 1.
 DR DR PRINTS; PR00024; HOMEBOX.
 DR DR SMART; SM00406; IgV; 1.
 DR DR PROSITE; PS50835; Ig_LIKE; 2.
 DR DR NON_TER 1 1
 FT FT NON_TER 214 214
 SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match, Best Local Similarity 97.0%; Score 546; DB 2; Length 214; Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIKMQPSMSMYASIGERVTICKASODINSLWFOQPKPSKPKLIVYRANLVDGVPS 60
 Db 1 DIKTQSSSSMSYASIGERVTICKASODINSLWFOQPKPSKPKLIVYRANLVDGVPS 60

QY 61 RFSGSGSGQDYSLTISLEVEYEDMGIVYCLQDEFPTFGGTKLK 107
 Db 61 RFSGSGSGQDYSLTISLEVEYEDMGIVYCLQDEFPTFGGTKLK 107

RESULT 3
 KV5P_MOUSE ID KV5P_MOUSE
 ID _KV5P_MOUSE STANDARD; PRT; 128 AA.
 AC P01637; DT 21-JUL-1985 (Rel. 01, Created)
 DR 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DR Ig kappa chain V-V region TI precursor
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] DR SEQUENCE FROM N.A.
 RR DR MEDLINE=81220975; PubMed=6264318;
 RA Pech M., Hochtl J., Schnell H., Zachau H.G.;
 DR "Differences between germ-line and rearranged immunoglobulin v kappa
 RT coding sequences suggest a localized mutation mechanism.";
 RL Nature 241:669-670 (1981).
 DR PIR; A01921; KUML6
 DR HSSP; P01607; IBWW.
 DR InterPro; IPR007110; Ig-like.
 DR IntePro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 KW Immunglobulin V region; Signal.
 FT FT SIGNAL 1 20
 FT CHAIN 21 >15 Ig kappa chain V-V region 16.
 FT DOMAIN 21 43 Framework-1.
 FT DOMAIN 44 54 Complementarity-determining-1.
 FT DOMAIN 55 69 Framework-2.
 FT DOMAIN 70 76 Complementarity-determining-2.
 FT DOMAIN 77 108 Framework-3.
 FT DOMAIN 109 >115 Complementarity-determining-3.
 FT DISULFID 43 108 BY similarity.
 SQ SEQUENCE 115 AA; 12986 MW; BA52C58F328E1C3 CRC64;

Query Match, Best Local Similarity 96.3%; Score 546; DB 2; Length 128; Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIKMQPSMSMYASIGERVTICKASODINSLWFOQPKPSKPKLIVYRANLVDGVPS 60
 Db 21 DIKMQPSMSMYASIGERVTICKASODINSLWFOQPKPSKPKLIVYRANLVDGVPS 60

QY 61 RFSGSGSGQDYSLTISLEVEYEDMGIVYCLQDEFPTFGGTKLK 107
 Db 81 RFSGSGSGQDYSLTISLEVEYEDMGIVYCLQDEFPTFGGTKLK 127

RESULT 4
 KV5P_MOUSE ID KV5P_MOUSE
 ID _KV5P_MOUSE STANDARD; PRT; 115 AA.
 AC P01638; DT 21-JUL-1986 (Rel. 01, Created)
 DR 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DR Ig kappa chain V-V region L6 precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] DR SEQUENCE FROM N.A.
 RR DR MEDLINE=81220975; PubMed=6264318;
 RA Pech M., Hochtl J., Schnell H., Zachau H.G.;
 DR "Differences between germ-line and rearranged immunoglobulin v kappa
 RT coding sequences suggest a localized mutation mechanism.";
 RL Nature 241:669-670 (1981).
 DR PIR; A01921; KUML6
 DR HSSP; P01607; IBWW.
 DR InterPro; IPR007110; Ig-like.
 DR IntePro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 KW Immunglobulin V region; Signal.
 FT FT SIGNAL 1 20
 FT CHAIN 21 >15 Ig kappa chain V-V region 16.
 FT DOMAIN 21 43 Framework-1.
 FT DOMAIN 44 54 Complementarity-determining-1.
 FT DOMAIN 55 69 Framework-2.
 FT DOMAIN 70 76 Complementarity-determining-2.
 FT DOMAIN 77 108 Framework-3.
 FT DOMAIN 109 >115 Complementarity-determining-3.
 FT DISULFID 43 108 BY similarity.
 SQ SEQUENCE 115 AA; 12986 MW; BA52C58F328E1C3 CRC64;

Query Match, Best Local Similarity 88.6%; Score 499; DB 1; Length 115;

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announce/> or send an email to license@ebi.ac.uk).
 EMBL; V00772; CAM24150.1; -. DR PIR; A01920; KVMS1L.

Best Local Similarity 100.0%; Pred. No. 4.5e-44; Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Db
QY	1 DIKMQSPASSWYSASIGERVTITCKASQDINSYLWFOQKQGKSRTKLIVANRLDGVS 60	Db
Db	21 DIKMQSPASSWYSASIGERVTITCKASQDINSYLWFOQKQGKSRTKLIVANRLDGVS 80	Db
QY	61 RFSGSGSGDYSLTISLEYEDMGIVYCYLQYDEFP 95	61 RFSGSGSGDYSLTISLEYEDMGIVYCYLQYDEFP 107
Db	81 RFSGSGSGDYSLTISLEYEDMGIVYCYLQYDEFP 115	83 RFSGSGSGDYSLTISLEYEDMGIVYCYLQYDEFP 129
RESULT 5		RESULT 6
Q7TMK3	PRELIMINARY; PRT; 236 AA.	KV1Y HUMAN STANDARD; PRT; 108 AA.
ID	Q7TMK3; DT 01-OCT-2003 (Tremblrel. 25, Created)	ID KV1Y HUMAN STANDARD; PRT; 108 AA.
AC	DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)	AC P803162;
DT	DT 01-OCT-2004 (Tremblrel. 26, Last annotation update)	DT 01-NOV-1995 (Rel. 32, Created)
DB	Hypothetical protein.	DT 01-OCT-2004 (Rel. 45, Last annotation update)
OS	Mus musculus (Mouse).	DE Ig kappa chain V-I region WAT.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [1]	OS Homo sapiens (Human)
OC	Mammalia; TairID=10090; NCBI_TaxID=9606;	OC Homo sapiens (Human)
OX		OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN		RN NCBI_TaxID=9606;
RP	SEQUENCE FROM N.A.	RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RC	STRAIN=CZECH II;	RC MEDLINE:22389257; PubMed=12477932;
RC	TISSUE=Hamartoma tumor metastatized to lung. Tumor arose spontaneously;	RC MEDLINE:9508080; PubMed=7993911;
RX	MEDLINE:22389257; PubMed=12477932;	RX Huang D.-B., Chang C.-H., Bruenger A.T., Bulitz M., Solomon A., Stevens F.J., Schiffer M., Solomon A., Stevens F.J., Schiffer M.; "Comparison of crystal structures of two homologous proteins: structural origin of altered domain interactions in immunoglobulin light-chain dimers"; Biichemistry 33:14848-14857(1994).
RA	Strausberg R.L., Ringold B.A., Grouse L.H., Dege J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Atschul S.P., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan B., Moore T., Max S.I., Wang J., Hsieh P., Blatchko L., Marusina K., Farmer A.A., Rubin G.M., Hong D., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uzdin B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Botak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H., Richards S., McElroy C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heitton E., Ketteman M., Rodriguez S., Sanchez A., RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Tschirman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smaluu D.E., Schnurch A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [2]	RA RX Stevens F.J., Westholm P.A., Panagiotopoulos N., Schiffer M., Popp R.A., Solomon A.; "Characterization and preliminary crystallographic data on the VL-related fragment of the human kI Bence Jones protein Wat"; J. Mol. Biol. 147:185-193(1981).
RA	RA -1 MISCELLANEOUS: This is a Bence-Jones protein.	RA DR PDB; 1WTL; X-ray; A/B-1-108
RA	RA GO; GO:0005576; C: extracellular; NAS.	DR GO; GO:0005576; C: extracellular; NAS.
RA	RA GO; GO:0003823; F: antigen binding; NAS.	DR GO; GO:0006555; P: immune response; NAS.
RA	RA DR InterPro; IPR007110; Ig-like.	DR InterPro; IPR003396; Ig_v.
RA	RA PFAM; PF00047; Ig_v.	DR SMART; SM00466; Ig_v; 1.
RA	RA PROSITE; PS00833; Ig_LIKE; 1.	DR PROSITE; PS00833; Ig_LIKE; 1.
RT	RT KW 3D-structure; Bence-Jones protein; direct protein sequencing; Immunoglobulin V region.	RT KW Immunoglobulin V region.
RL	RL STRAIN=CZECH II;	FT DOMAIN 1 Framework-1.
RC	RC TISSUE=Hamartoma tumor metastatized to lung. Tumor arose spontaneously;	FT DOMAIN 2 Framework-complementarity-determining-1.
RA	RA Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.	FT DOMAIN 3 Framework-complementarity-determining-2.
RA	RA STRAUSBERG R.; EMBL; BC055906; AAC55906_1; -.	FT DOMAIN 5 Framework-complementarity-determining-3.
DR	DR InterPro; IPR007110; Ig-like.	FT DOMAIN 89 Framework-4.
DR	DR InterPro; IPR033597; Ig_cI.	FT DOMAIN 98 By similarity.
DR	DR InterPro; IPR003006; Ig_MHC.	FT DOMAIN 56 TN -> SD (in Ref. 2).
DR	DR InterPro; IPR003566; Ig_v.	FT DOMAIN 57
DR	DR PFAM; PF07654; Cl_Bet; T.	FT DOMAIN 89 Framework-3.
DR	DR SMART; SM00466; Ig_v; 1.	FT DOMAIN 97 Complementarity-determining-3.
DR	DR PROSITE; PS00833; Ig_LIKE; 2.	FT DOMAIN 98 Framework-4.
DR	DR PROSITE; PS00090; Ig_MHC; UNKNOWN_1.	FT DOMAIN 99 By similarity.
KW	KW Hypothetical protein.	FT DOMAIN 10 TN -> SD (in Ref. 2).
SQ	SQ SEQUENCE 236 AA; 26299 MW; ODB03488AA6396F CRC64;	FT TURN 13 STRAND 10 Framework-1.
QY	Query Match 83.1%; Score 468; DB 2; Length 236; Best Local Similarity 85.0%; Pred. No. 1.8e-40; Matches 91; Conservative 3; Mismatches 13; Indels 0; Gaps 0;	FT TURN 15 STRAND 10 Framework-complementarity-determining-1.
QY	1 DIKMQSPASSWYSASIGERVTITCKASQDINSYLWFOQKQGKSRTKLIVANRLDGVS 60	FT TURN 25 STRAND 19 Framework-complementarity-determining-2.
QY	21 DIKMQSPASSWYSASIGERVTITCKASQDINSYLWFOQKQGKSRTKLIVANRLDGVS 80	FT TURN 31 STRAND 30 Framework-complementarity-determining-3.
QY	61 RFSGSGSGDYSLTISLEYEDMGIVYCYLQYDEFP 95	FT TURN 38 STRAND 33 By similarity.
QY	81 RFSGSGSGDYSLTISLEYEDMGIVYCYLQYDEFP 115	FT TURN 41 STRAND 4 TN -> SD (in Ref. 2).
QY	61 RFSGSGSGDYSLTISLEYEDMGIVYCYLQYDEFP 107	FT TURN 49 STRAND 10 Framework-4.
QY	83 RFSGSGSGDYSLTISLEYEDMGIVYCYLQYDEFP 129	FT TURN 52 STRAND 54 By similarity.

FT HELIX 80 82
 FT STRAND 84 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT NON TER 108 108
 SQ 108 AA; 11737 MW; D9D941B3P0AB697 CRC64;

Query Match 70.7%; Score 398; DB 1; Length 108;
 Best Local Similarity 68.2%; Pred. No. 1 4e-33;
 Matches 73; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

QY 1 DIKOTQSSISMSVYSLGERVTICKASODINSYLSWQOKPKSKLILYRANKLVGVPs 60
 1 DQMQTSPSSLSASVGDRVTICASODINTYVNWFOQRPSQAKPLIYASILETGVPs 60
 Db 61 RPSGSGSQDYSLTSSLEVEDMGIVCLQDYDEPFYFFGGTKLEI 107
 61 RPSGSGSQDYSLTSSLEVEDMGIVCLQDYDEPFYFFGGTKLEI 107

RESULT 7

KYLO_HUMAN	STANDARD	PRT	108 AA.
ID P01607; 21-JUL-1986 (Rel. 01, Created)			
DT 01-OCT-2004 (Rel. 45, Last sequence update)			
DE Ig kappa chain V-I region Ref.			
OS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buterria; Primates; Catarrhini; Hominidae; Homo. [1]			
OX NCBI_TaxID=9605; RNAME=P01607; SEQUENCE:			
RN 1136039868; PubMed=1122131; MEDLINE=76023758; PubMed=809329; RNAME=P01607; SEQUENCE:			
RA Palm W., Hilschmann N.; "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Ref), isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site." Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).			
RL X-RAY CRYSTALLOGRAPHY (12.0 ANGSTROMS). RNAME=P01607; SEQUENCE:			
RA Epp O., Lattman E.B., Schiffer M., Huber R., Palm W.; "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein Ref refined at 2.0-A resolution.", Biochemistry 14:4943-4952(1975).			
CC -1 MISCELLANEOUS: This is a Bence-Jones protein. marker.			
CC DR PIR: A91663; KIHUEC: DR; PDB: 1ARZ; X-ray; @=1-107. DR; PDB: 1BMW; X-ray; A/B=1-107. DR; PDB: 1R37; X-ray; A/B=1-107. DR; GO: GO:000323; Plantigen binding; NAS. GO: GO:000655; P: immune response; NAS. InterPro: IPR007110; Ig-like. InterPro: IPR003196; Ig_v. InterPro: IPR003196; Ig_v. Pfam: PRO0047; Ig_v. SMART: SW00046; IgV; 1. PROSITE: PS00835; Ig_LIKE; 1. KW 3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region. DOMAIN 1 23 Framework-1. DOMAIN 24 34 Complementarity-determining-1. DOMAIN 35 49 Framework-2. DOMAIN 50 56 Complementarity-determining-2. DOMAIN 57 89 Framework-3. DOMAIN 89 97 Complementarity-determining-3.			

RESULT 7

KYLO_HUMAN	STANDARD	PRT	108 AA.
ID P01607; 21-JUL-1986 (Rel. 01, Created)			
DT 01-OCT-2004 (Rel. 45, Last sequence update)			
DE Ig kappa chain V-I region Ref.			
OS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buterria; Primates; Catarrhini; Hominidae; Homo. [1]			
OX NCBI_TaxID=9605; RNAME=P01607; SEQUENCE:			
RN 1136039868; PubMed=1122131; MEDLINE=76023758; PubMed=809329; RNAME=P01607; SEQUENCE:			
RA Palm W., Hilschmann N.; "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Ref), isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site." Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).			
RL X-RAY CRYSTALLOGRAPHY (12.0 ANGSTROMS). RNAME=P01607; SEQUENCE:			
RA Epp O., Lattman E.B., Schiffer M., Huber R., Palm W.; "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein Ref refined at 2.0-A resolution.", Biochemistry 14:4943-4952(1975).			
CC -1 MISCELLANEOUS: This is a Bence-Jones protein. marker.			
CC DR PIR: A91663; KIHUEC: DR; PDB: 1ARZ; X-ray; @=1-107. DR; PDB: 1BMW; X-ray; A/B=1-107. DR; PDB: 1R37; X-ray; A/B=1-107. DR; GO: GO:000323; Plantigen binding; NAS. GO: GO:000655; P: immune response; NAS. InterPro: IPR007110; Ig-like. InterPro: IPR003196; Ig_v. InterPro: IPR003196; Ig_v. Pfam: PRO0047; Ig_v. SMART: SW00046; IgV; 1. PROSITE: PS00835; Ig_LIKE; 1. KW 3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region. DOMAIN 1 23 Framework-1. DOMAIN 24 34 Complementarity-determining-1. DOMAIN 35 49 Framework-2. DOMAIN 50 56 Complementarity-determining-2. DOMAIN 57 89 Framework-3. DOMAIN 89 97 Complementarity-determining-3.			

RESULT 8

KYLO_HUMAN	PRELIMINARY	PRT	236 AA.
ID Q723Y4; 01-OCT-2003 (TREMBLrel. 25, Created)			
AC Q723Y4; 01-OCT-2003 (TREMBLrel. 25, Last sequence update)			
CC DE Hypothetical protein.			
CC OS Homo sapiens (Human)			
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buterria; Primates; Catarrhini; Hominidae; Homo. [1]			
CC OX NCBI_TaxID=9606; RNAME=Q723Y4; SEQUENCE FROM N.A.			
CC TISSUE=Skeletal Muscle; MEDLINE=2238257; RNAME=Q723Y4; PRELIMINARY; PRT; 236 AA.			
CC DR Strauberg R.L., Feingold E.B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemer C.M., Schuler G.D., Altshull S.P., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heile F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullahay S.J., Pfan P.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.J., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heitton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.B., Dickson M.C., RA Borak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.J., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A., RA FAHEY J., HEITTON E., KETTEMAN M., MADAN A., RODRIGUES S., SANCHEZ A., RA WHITING M., MADAN A., YOUNG A.C., SHEVCHENKO I., BOUFFARD G.G., RA RODRIGUEZ A.C., GRIMWOOD J., SCHMITZ J., MYERS J., GAY L.J., BUTTERFIELD Y.S., RA KRYWIANSKI M.I., SKALSKA U., SMALIBUS D.E., SCHENCK A., SCHEIN J.E., RA JONES S.J., MARZA M.A., RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", PROC. NATL. ACAD. SCI. U.S.A. 99:16899-16903 (2002).			

RESULT 8

KYLO_HUMAN	PRELIMINARY	PRT	236 AA.
ID Q723Y4; 01-OCT-2003 (TREMBLrel. 25, Created)			
AC Q723Y4; 01-OCT-2003 (TREMBLrel. 25, Last sequence update)			
CC DE Hypothetical protein.			
CC OS Homo sapiens (Human)			
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buterria; Primates; Catarrhini; Hominidae; Homo. [1]			
CC OX NCBI_TaxID=9606; RNAME=Q723Y4; SEQUENCE FROM N.A.			
CC TISSUE=Skeletal Muscle; MEDLINE=2238257; RNAME=Q723Y4; PRELIMINARY; PRT; 236 AA.			
CC DR Strauberg R.L., Feingold E.B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemer C.M., Schuler G.D., Altshull S.P., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heile F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullahay S.J., Pfan P.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.J., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heitton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.B., Dickson M.C., RA Borak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.J., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A., RA FAHEY J., HEITTON E., KETTEMAN M., MADAN A., RODRIGUES S., SANCHEZ A., RA WHITING M., MADAN A., YOUNG A.C., SHEVCHENKO I., BOUFFARD G.G., RA RODRIGUEZ A.C., GRIMWOOD J., SCHMITZ J., MYERS J., GAY L.J., BUTTERFIELD Y.S., RA KRYWIANSKI M.I., SKALSKA U., SMALIBUS D.E., SCHENCK A., SCHEIN J.E., RA JONES S.J., MARZA M.A., RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", PROC. NATL. ACAD. SCI. U.S.A. 99:16899-16903 (2002).			

RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE-skeletal Muscle;
RA	Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RL	EMBL; BC005322; AAH05322; 1; -.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR03066; Ig_MHC.
DR	InterPro; IPR03396; Ig_v.
DR	Pfam; PF07654; Cl-set_1.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SM00406; Ig_V.
DR	PROSITE; PS00835; Ig_LIKE; 2.
DR	PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
KW	Hypothetical protein.
SQ	SEQUENCE 236 AA; 25702 MW; 7FBFEBD23084BC6 CRC64;
Query Match	70.0%; Score 394; DB 2; Length 236; Best Local Similarity 69.2%; Pred. No. 9e-33; Conservative 16; Mismatches 17; Indels 0; Gaps 0;
Oy	1 DIKOMTOSPSMYASIGERVITICKASQDINSYLSWFOOKPGKSKPTLYRANRLVGVPS 60
Db	23 DIQMTQSPSSILASAVGDTWVITCKASQDINSYLNWFOOKPGKAKRSKLIGASSLGVS 82
Oy	61 RFSGSGSGQDYSLTISLSEEDMGIVYCLQDYDERPYTGGGKLEIK 107
Db	83 KFGSGGSGDFTLTISLQPEDRATYYCQKYKVTFQGTKLKIK 129
RESULT 9	KV1B_HUMAN STANDARD; PRT; 108 AA.
ID	KV1B_HUMAN
AC	P01594;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	01-OCT-2004 (Rel. 45, last annotation update)
DE	IG kappa chain V-I region AU.
OS	Homo sapiens (Human).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID:9606;
RN	[1]
RP	SEQUENCE.
RX	Medline=72189444; PubMed=5028201;
RA	Schiebel H., Hilchmann N.;
RR	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au)"; Z. Physiol. Chem. 353:345-370(1972).
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RP	X-RAY CRYSTALLOGRAPHY.
RX	Medline=77022433; PubMed=1234024;
RA	Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman B.E., Schwager P., Steigemann W., Schramm H.J.;
RR	"The structure determination of the variable portion of the Bence-Jones protein Au"; J. Physiol. Chem. 246:149-155(1975).
RL	Biophys. Struct. Mech. 1:139-146(1975).
CC	- MISCCELLANEOUS: The structure of the V region was determined by molecular replacement methods using the known structure of the V region of the kappa chain REG.
CC	- MISCCELLANEOUS: This is a Bence-Jones protein.
CC	- MISCCELLANEOUS: The C region of this chain has the INV (3) marker.
CC	PIR; A91653; KIUMAU.
CC	PDB; 1JUV; X-ray; A=1-107.
CC	C:extracellular; NAS.
CC	GO; GO:0005823; P:antigen binding; NAS.
CC	GO; GO:0006555; P:immune response; NAS.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR03596; Ig_v.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SM00406; Ig_V.
DR	PROSITE; PS00835; Ig_LIKE; 1.
DR	PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
DR	Hypothetical protein.
DR	SEQUENCE FROM N.A.
RX	Medline=98277139; PubMed=9614934;
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Benney S.M., Young D.C.;
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.," Clin. Immunol. Immunopathol. 87:184-197(1998).
DR	EMBL; AF035044; AD56280.1; -.
DR	PIR; PH0863; PH0863.
DR	HSSP; P01607; IBMW.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR03596; Ig_v.
DR	Pfam; PF00047; Ig_1.

			RN [1]
Db	23	DIQWTOQSPSSVSASVGDRTTICRASOGISWLNQYQKKGAKPLIYHASSLQGVPS 82	SEQUENCE FROM N.A.
Qy	61	RFSGSGSGQDYSLSLEBDMGIVYCLQYDEPPYTFGGTKLEIK 107	RC TISSUE=Primary B-Cells;
Db	83	RFSGSGSGTPTLTSSLSQEDFATYQCOQHSPPTFGCTKVIK 129	RC MEDLINE=2238857; PubMed=12477932;
RESULT 13	KV1V_HUMAN	KV1V_HUMAN STANDARD; PRT; 108 AA.	RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Dierig J.C., Schuler G.D., Bhat N.K., Shemesh G.M., Hsieh P., Kleinman R.D., Jordan H., Moore T., Max S.I., Wang J.J., Hong L., Buetow K.H., Schaefer C.P., Bhat N.K., Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh P., Diachenko L., Marcus K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Raba S.S., Louvello N.A., Peters G.J., Abramson R.D., Mallay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fathhey J., Heitton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whaling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.B., Schnurch A., Schein J.E., Jones S.J., Marr M.A.,
SEQUENCE		Homo sapiens (Human); Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Homidae; Homo. [1]_TaxID=9606;	RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RA	Dwight P.E.; O'Connor T.P.; Benson M.D.; RT "Polymorphism in a kappa I primary (Al) amyloid protein (BAN)." ; Mol. Immunol. 23:71-78(1986).	RL RN [2]	
RL	DR HSPB; P0352; IWL.	RP TISSUE=PRIMRY B-cells;	
DR	GO; GO:0005576; C:extracellular; NAS.	RA Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	
DR	GO; GO:0006955; P:immune response; NAS.	DR EMBL; BC073763; ABH73763; 1; -.	
DR	GO; GO:0007110; Ig-like.	DR InterPro; IPR003559; Ig.	
DR	InterPro; IPR003595; Ig_v.	DR InterPro; IPR007110; Ig-like.	
DR	Pfam; PF00047; Ig; 1.	DR InterPro; IPR003597; Ig_c1.	
DR	SMART; SM00405; IgV; 1.	DR InterPro; IPR003006; Ig_MHC.	
DR	PROSITE; PS50835; Ig_LIKE; 1.	DR InterPro; IPR003556; Ig_v.	
KW	amyloid; Direct protein sequencing; Immunoglobulin V region.	DR Pfam; PF00047; Ig; 1.	
FT	DOMAIN 1 23 Framework-1.	DR Pfam; PF00047; Ig; 2.	
FT	DOMAIN 24 34 Complementarity-determining-1.	DR SMART; SM00409; Ig; 2.	
FT	DOMAIN 35 49 Framework-2.	DR SMART; SM00407; IgC1; 1.	
FT	DOMAIN 50 56 Complementarity-determining-2.	DR SMART; SM00406; IgV; 1.	
FT	DOMAIN 57 88 Framework-3.	DR PROSITE; PS50835; Ig_LIKE; 2.	
FT	DOMAIN 89 97 Complementarity-determining-3.	DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.	
FT	DOMAIN 98 107 Framework-4.	DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.	
FT	DISULFID 23 88 By similarity.	DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.	
FT	NON_TER 108 108 SEQUENCE 108 AA; 11840 MW; CD3FD94FFE96FD37 CRC64;	DR Hypothetical protein.	
SQ	Query Match 68.9%; Score 388; DB 1; Length 108; Best Local Similarity 65.4%; Pred. No. 1.5e-32; Matches 70; Conservative 20; MisMatches 17; Indels 0; Gaps 0;	SEQUENCE 236 AA; 25924 MW; FDB2093DC560CPFT CRC54;	
Qy	1 DIKOMTQSPSSMYASIGERVITCKASQDINSYLSWFOOKPKGSKPKNLTYRANLVDGVPS 60	Query Match 68.2%; Score 384; DB 2; Length 236; Best Local Similarity 65.4%; Pred. No. 9.9e-32; Matches 70; Conservative 20; MisMatches 17; Indels 0; Gaps 0;	
Db	1 DIQUTQSPSSLSASIGDRVITCRASQSYINVAWFQQEKAPKSLIDASTLQSGVPS 60	Qy 1 DIKOMTQSPSSMYASIGERVITCKASQDINSYLSWFOOKPKGSKPKNLTYRANLVDGVPS 60	
Qy	61 RFSGSGSGDYSLSLEBDMGIVYCLQYDEPPYTFGGTKLEIK 107	Db 23 DIQUTQSPSSLSASIGDRVITCRASQSYINVAWFQQEKAPKSLIDASTLQSGVPS 62	
Db	61 NFTUGSGSGTDPILTISLQEDFATYQCOQNTYPLTFGGTKVEIK 107	Qy 61 RFSGSGSGDYSLSLEBDMGIVYCLQYDEPPYTFGGTKLEIK 107	
RESULT 14	KV1_HUMAN	KV1_HUMAN STANDARD; PRT; 108 AA.	Db 83 RFSGSGSGTPTLTSSLSQEDFATYQCOQNTYPLTFGGTKVEIK 129
Q6GX9	ID Q6GX9 PRELIMINARY; PRT; 236 AA.	RESULT 15	
AC	Q6GX9; DT 05-JUL-2004 (Tremblel. 27, Last sequence update)	ID KV1_HUMAN	
DT	05-JUL-2004 (Tremblel. 27, Last annotation update)	AC P01610; DT 21-JUL-1986 (Rel. 01, Created)	
DT	Hypothetical protein.	DT 21-JUL-1986 (Rel. 01, Last sequence update)	
OS	Homo sapiens (Human).	DT 05-JUL-2004 (Rel. 44, Last annotation update)	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Homidae; Homo.	DR Ig kappa chain V-I region WEA.	
OX	NCBI_TaxID=9606;	OS Homo sapiens (Human).	
OX		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Homidae; Homo.	
OX		OX NCBI_TaxID=9606;	
OX		RN [1]	
		SEQUENCE FROM N.A.	
		RC TISSUE=Primary B-Cells;	
		RC MEDLINE=2238857; PubMed=12477932;	
		RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Dierig J.C., Schuler G.D., Bhat N.K., Shemesh G.M., Hsieh P., Kleinman R.D., Jordan H., Moore T., Max S.I., Wang J.J., Hong L., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh P., Diachenko L., Marcus K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Raba S.S., Louvello N.A., Peters G.J., Abramson R.D., Mallay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fathhey J., Heitton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whaling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.B., Schnurch A., Schein J.E., Jones S.J., Marr M.A.,	
		RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
		RL RN [2]	
		RP TISSUE=PRIMRY B-cells;	
		RA Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	
		DR EMBL; BC073763; ABH73763; 1; -.	
		DR InterPro; IPR003559; Ig.	
		DR InterPro; IPR007110; Ig-like.	
		DR InterPro; IPR003597; Ig_c1.	
		DR InterPro; IPR003006; Ig_MHC.	
		DR InterPro; IPR003556; Ig_v.	
		DR Pfam; PF00047; Ig; 1.	
		DR Pfam; PF00047; Ig; 2.	
		DR SMART; SM00409; Ig; 2.	
		DR SMART; SM00407; IgC1; 1.	
		DR SMART; SM00406; IgV; 1.	
		DR PROSITE; PS50835; Ig_LIKE; 2.	
		DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.	
		DR Hypothetical protein.	
		SEQUENCE 236 AA; 25924 MW; FDB2093DC560CPFT CRC54;	
		Query Match 68.2%; Score 384; DB 2; Length 236; Best Local Similarity 65.4%; Pred. No. 9.9e-32; Matches 70; Conservative 20; MisMatches 17; Indels 0; Gaps 0;	
		Qy 1 DIKOMTQSPSSMYASIGERVITCKASQDINSYLSWFOOKPKGSKPKNLTYRANLVDGVPS 60	
		Db 23 DIQUTQSPSSLSASIGDRVITCRASQSYINVAWFQQEKAPKSLIDASTLQSGVPS 62	
		Qy 61 RFSGSGSGDYSLSLEBDMGIVYCLQYDEPPYTFGGTKLEIK 107	
		Db 83 RFSGSGSGTPTLTSSLSQEDFATYQCOQNTYPLTFGGTKVEIK 129	

RA
 RT
 "Amino acid sequence of the Fv region of a human monoclonal IgM
 (protein WE) with antibody activity against 3,4-pyruvylated galactose
 in Klebsiella polybaccarides K30 and K33";
 Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC
 -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody with
 against 3,4-pyruvylated galactose and isolated from a patient with
 Waldenstrom's macroglobulinemia.
 DR
 PIR: A01876; KIHWE.
 DR
 HSSP; P80362; IgV.
 DR
 GO; GO:0005576; C:extracellular; NAS.
 DR
 GO; GO:0003923; F:antigen binding; NAS.
 DR
 GO:0005955; P:immune response; NAS.
 DR
 InterPro; IPR007110; Ig-like.
 DR
 Pfam; PF00047; Ig_v.
 SMART; SW00406; IgV; 1.
 DR
 PROSITE; PS0835; IG_LIKE; 1.
 KW
 direct protein sequencing; Immunoglobulin V region;
 KW
 Monoclonal antibody.
 FT
 DOMAIN 1 23 Framework-1.
 FT
 DOMAIN 24 34 Complementarity-determining-1.
 FT
 DOMAIN 35 49 Framework-2.
 FT
 DOMAIN 50 56 Complementarity-determining-2.
 FT
 DOMAIN 57 88 Framework-3.
 FT
 DOMAIN 89 97 Complementarity-determining-3.
 FT
 DOMAIN 98 107 Framework-4.
 FT
 DISULFID 23 88 By similarity.
 FT
 NON_TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61R0945618C CRC64;
 Query Match 68.0%; Score 383; DB 1; Length 108;
 Best Local Similarity 66.4%; Pred. No. 5.1e-32; Gaps 0;
 Matches 71; Conservative 17; Mismatches 19; Indels 0; Gaps 0;
 Qy 1 DIKMTQSPSMSVAKSLGERVITCKASQDINSYLSWFOQQKGKSPKTLIYRNRLVDGVS 60
 Db 1 DIOMTQSPSISASVGDVITCRASQDINSYLSWFOQQKGKSPKTLIYRNRLVDGVS 60
 Qy 61 RFSGSSGQDYSLTSSLSEYEDMGIVYCYCLODERPYTFCGGTKHIK 107
 Db 61 RFSGSSGQDYSLTSSLSEYEDMGIVYCYCLODERPYTFCGGTKHIK 107

Search completed: December 29, 2004, 18:05:18
 Job time : 75.8584 SECs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:46:45 ; Search time 14.677 seconds

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0 (without alignments)
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:
 1: Pir1;
 2: pir2;
 3: Pir3;
 4: pir4;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	546	97.0	127	SS2447
2	534	94.8	128	1 KWMST1
3	525	93.3	234	S14237
4	519	92.2	128	PL0101
5	505	89.9	106	S20552
6	499	88.6	115	1 KWSL6
7	487	86.5	98	PH1065
8	460	81.7	104	2 S1370
9	440	78.2	103	2 S13703
10	412	73.2	129	B23986
11	410	72.8	101	2 S13701
12	410	72.8	129	2 S52789
13	399	70.9	2 A34966	
14	397	70.5	107	2 S32624
15	397	70.5	129	2 S40369
16	397	70.5	132	2 S40334
17	395	70.2	125	2 S40316
18	394	70.0	108	1 KHRB
19	394	70.0	125	2 S40333
20	393	69.8	108	1 KIHUAU
21	393	69.8	108	2 I39154
22	393	69.8	108	2 B49047
23	392.5	69.7	106	2 C3396
24	392	69.6	108	2 S19674
25	391	69.4	108	1 KIHUR
26	389	69.1	123	2 S40313
27	389	69.1	131	2 S40352
28	388.5	69.0	104	2 S26329
29	388	68.9	108	1 KIHUB

ALIGMENTS

RESULT 1							
Query	Match	Best Local Similarity	Score	DB	ID	Length	Description
SS2447	Ig kappa chain V region - mouse	95.3%	546	DB 2;	SS2447	127;	
	CSpecies: Mus musculus (house mouse)						
	CDate: 08-May-1995 #Sequence_revision 21-Jul-1995 #text_change 21-Jan-2000						
	CAccession: S52447						
	R: Berdoz, J.; Krechenbuhl, J.-P.						
	submitted to the EMBL Data library, November 1994						
	A: Description: Specific amplification by the polymerase chain reaction of rearranged genes						
	A: Reference number: S52445						
	A: Accession: S52447						
	A: Status: preliminary						
	A: Molecule type: DNA						
	A: Residues: 1-127 <BER>						
	A: Cross-references: EMBL:X82688; NID:9673443; PIDN:CAA58009.1; PID:9673444						
	C: Genetics:						
	A: Introns: 17/1						
	C: Superfamily: immunoglobulin V region; immunoglobulin homology						
	C: Keyword: heterotetramer; immunoglobulin Fc36-110/Domain: immunoglobulin homology <IMM>						
	Query Match Best Local Similarity 97.0%; Score 546; DB 2; Length 127; Matches 102; Conservative 5; Mismatches 0; Indels 0; Gaps 0;						
	OY	1	DIKMTQSSSMYASLGERVTICKASODINTSYLSWFOOKPGKSPRTLIVRANRLVGDVPS	Db	21	60	
	OY	1	DIKMTQSSSMYASLGERVTICKASODINTSYLSWFOOKPGKSPRTLIVRANRLVGDVPS	Db	21	80	
	61 RSGSGSGDYSLTISSLREYDMGIVYCYLOYDERPYTFCGGTKLEIK	61	107				
	81 RFSGSGSGDYSLTISSLREYDMGIVYCYLOYDERPYTFCGGTKLEIK	81	127				
	KWMST1						
	Ig kappa chain precursor V region (TR1) - mouse						
	C:Species: Mus musculus (house mouse)						
	C:Date: 13-Dec-1980 #Sequence_revision 08-Oct-1981 #text_change 09-Jul-2004						
	CAccession: A01920						
	R: Altenburger, W.; Steinmetz, M.; Zachau, H.G.						
	Nature 287, 603-607, 1980						
	A: Title: Functional and non-functional joining in immunoglobulin light chain genes of a						
	A: Reference number: A01920; MUID:81052342; PMID:6776411						
	A: Accession: A01920						
	A: Molecule type: mRNA						
	A: Residues: 1-128 <ALT>						
	A: Cross-references: EMBL:P01637; GB:v00772; NID:951536; PIDN:CAA24150.1; PID:9762975						
	A: Note: the sequence was determined from the differentiated gene						
	C: Genetics:						
	A: Introns: 17/1						
	C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka						

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer

F;1-2/Domain: signal sequence #status predicted <SIG>

F;21-110/Product: Ig kappa chain V region (m) #status predicted <MAT>

F;43-108/Disulfide bonds: #status predicted

Query Match 1 DIKMTQSPSSMVASLGERVTICKASQDINSYLSFQQPKGSKPLTYRANRLVGDVS

Best Local Similarity 93.5%; Pred. No. 1.7e-38; Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 21 DIKMTQSPSSMVASLGERVTICKASQDINSYLSFQQPKGSKPLTYRANRLVGDVS 60

Qy 61 RFSGSGSGQDYSLTISLEVEDMGIVYCYQDYDERPYTREGGTKEIK 107

Db 81 RFSGSGSGQDYSLTISLEVEDMGIVYCYQDYDERPYTREGGTKEIK 127

RESULT 3 S14237

Ig kappa chain precursor (15G5) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S14237 R;Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.

Eur. J. Biochem. 192, 767-775, 1990

A;Title: Construction and characterization of a recombinant murine monoclonal antibody d

A;Reference number: S14236; MUID:91006173; PMID:2209622

A;Accession: S14237 A;Residues: 1-234 <VAL>

A;Molecule type: mRNA

A;Cross-references: EMBL:X56394; NID:951622; PIDN:CAA39805_1; PID:951623

C;Key-words: heterotrimer; immunoglobulin V region; immunoglobulin homology <IMM>

Query Match 93.3%; Score 525; DB 2; Length 234; Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSSMVASLGERVTICKASQDINSYLSFQQPKGSKPLTYRANRLVGDVS 60

Db 21 DIKMTQSPSSMVASLGERVTICKASQDINSYLSFQQPKGSKPLTYRANRLVGDVS 80

Qy 61 RFSGSGSGQDYSLTISLEVEDMGIVYCYQDYDERPYTREGGTKEIK 107

Db 81 RFSGSGSGQDYSLTISLEVEDMGIVYCYQDYDERPYTREGGTKEIK 127

RESULT 5 S20652

Ig kappa chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C;Accession: S20652 R;Lozman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.

Submitted to the EMBL Data Library, February 1992

A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice reac

A;Reference number: S20639

A;Accession: S20652

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-106 <LOS>

A;Cross-references: EMBL:65008; NID:952649; PIDN:CAA46141_1; PID:952650

C;Key-words: heterotrimer; immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.9%; Score 506; DB 2; Length 106; Matches 95; Conservative 89.6%; Pred. No. 3.4e-36; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSSMVASLGERVTICKASQDINSYLSFQQPKGSKPLTYRANRLVGDVS 60

Db 1 DIKMTQSPSSMVASLGERVTICKASQDINSYLSFQQPKGSKPLTYRANRLVGDVS 80

Qy 61 RFSGSGSGQDYSLTISLEVEDMGIVYCYQDYDERPYTREGGTKEIK 106

Db 61 RFSGSGSGQDYSLTISLEVEDMGIVYCYQDYDERPYTREGGTKEIK 106

Db 81 RFSGSGSGQDYSLTISLEVEDMGIVYCYQDYDERPYTREGGTKEIK 127

RESULT 6 KM515

Ig kappa chain precursor V region (L6) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004

C;Accession: A01921 R;Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.

Nature 291, 668-670, 1981

A;Title: Differences between germline and rearranged immunoglobulin V-kappa coding seq

R;Nar, R.I.; Haber, E.

Mol. Immunol. 26, 371-382, 1989

A;Title: Characterization of the heavy and light chain immunoglobulin variable region 9c

A;Reference number: P0100; MUID:89238344; PMID:2497340

A;Accession: P0101

A;Molecule type: DNA

A;Residues: 1-128 <NEA>

A;Experimental source: strain A/J

A;Note: the sequence was determined from the germline gene

A;Residues: 1-128

A;Cross-references: UNIPROT:P01638; GB:V01563; GB:J00573; NID:951714; PIDN:CAA24883_1; 1

C;Genetics: 1/1

A;Introns: 1/1 <PEC>

A;Note: the sequence was determined from the germline gene

A;Introns: 1/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kai

C;Keywords: heterotetramer

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-115/Product: Ig kappa chain V region (L6) #status predicted <MAT>

F;36-110/Domain: immunoglobulin homology <IMM>

F;43-108/Disulfide bonds: #status predicted

F;36-110/Domain: immunoglobulin homology <IMM>

F;115-128/Domain: J segment #status predicted <JRB>

Query Match 1 DIKMTQSPSSMVASLGERVTICKASQDINSYLSFQQPKGSKPLTYRANRLVGDVS

Best Local Similarity 92.3%; Score 519; DB 2; Length 128; Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 21 DIKMTQSPSSMVASLGERVTICKASQDINSYLSFQQPKGSKPLTYRANRLVGDVS 60

Qy 61 RFSGSGSGQDYSLTISLEVEDMGIVYCYQDYDERPYTREGGTKEIK 107

Db 81 RFSGSGSGQDYSLTISLEVEDMGIVYCYQDYDERPYTREGGTKEIK 127

Query Match Similarity 88.6%; Score 499; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.4e-35; Mismatches 0; Indels 0; Gaps 0;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Db 21 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Qy 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 104
 Db 81 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 104

RESULT 7
 PH1065 Ig kappa chain V region (clone 163.47) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: PH1065
 R;Tillman, D.M.; Jon, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
 A;Reference number: PH0971; MUID:238144; PMID:151250
 A;Accession: PH1065
 A;Species: Mus musculus (house mouse)
 A;Residues: 1-98 <TIL>
 A;Cross-references: UNIPROT:OPRIAS5
 A;Experimental source: B cell, strain NZB x NZW/F1
 C;Superfamily: Immunoglobulin V region; immunoglobulin homology
 C;Keywords: Immunoglobulin

Query Match Similarity 86.5%; Score 487; DB 2; Length 98;
 Best Local Similarity 94.9%; Pred. No. 1.3e-34; Mismatches 4; Indels 0; Gaps 0;
 Matches 93; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Db 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Qy 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 98
 Db 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 98

RESULT 8

S13700 Ig kappa chain V region (hybridoma NC19-E10) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S13700; S13702

R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

Eur. J. Immunol. 19, 1289-1295, 1989

A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clonal selection

A;Reference number: S13685; MUID:89338557; PMID:2503389

A;Accession: S13703

A;Species: preimmune

A;Molecule type: mRNA

A;Residues: 1-103 <PEN>

A;Cross-references: EMBL:X53356; MIM:955310; PID:CAA37442.1; PID:9930227

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetrabramer; immunoglobulin

F;1e-90/Domain: immunoglobulin homology <IMM>

RESULT 9

S13703 Ig kappa chain V region (hybridoma NC17-D8) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S13703

R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

Eur. J. Immunol. 19, 1289-1295, 1989

A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clonal selection

A;Reference number: S13685; MUID:89338557; PMID:2503389

A;Accession: S13703

A;Species: preimmune

A;Molecule type: mRNA

A;Residues: 1-103 <PEN>

A;Cross-references: EMBL:X53356; MIM:955310; PID:CAA37442.1; PID:9930227

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetrabramer; immunoglobulin

F;1e-90/Domain: immunoglobulin homology <IMM>

Query Match Similarity 78.2%; Score 440; DB 2; Length 103;

Best Local Similarity 83.3%; Pred. No. 1.3e-30; Mismatches 14; Indels 0; Gaps 0;

Matches 85; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Db 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Qy 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 102
 Db 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 102

Query Match Similarity 73.2%; Score 412; DB 2; Length 129;

Best Local Similarity 72.9%; Pred. No. 3.7e-28; Mismatches 18; Indels 0; Gaps 0;

Matches 78; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Db 23 DIKMTQSPSMSVSLDVTIPCRASQDQIVVWFOQPKGSKPRTLYLADGVPS 82
 Qy 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 107
 Db 83 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 129

Query Match Similarity 88.6%; Score 499; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.4e-35; Mismatches 0; Indels 0; Gaps 0;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Db 21 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Qy 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 104
 Db 81 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 104

RESULT 7
 PH1065 Ig kappa chain V region (clone 163.47) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: PH1065
 R;Tillman, D.M.; Jon, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
 A;Reference number: PH0971; MUID:238144; PMID:151250
 A;Accession: PH1065
 A;Species: Mus musculus (house mouse)
 A;Residues: 1-98 <TIL>
 A;Cross-references: UNIPROT:OPRIAS5
 A;Experimental source: B cell, strain NZB x NZW/F1
 C;Superfamily: Immunoglobulin V region; immunoglobulin homology
 C;Keywords: Immunoglobulin

Query Match Similarity 86.5%; Score 487; DB 2; Length 98;
 Best Local Similarity 94.9%; Pred. No. 1.3e-34; Mismatches 4; Indels 0; Gaps 0;
 Matches 93; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Db 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Qy 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 98
 Db 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 98

RESULT 8
 S13700 Ig kappa chain V region (hybridoma NC19-E10) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C;Accession: S13700; S13702

R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

Eur. J. Immunol. 19, 1289-1295, 1989

A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clonal selection

A;Reference number: S13685; MUID:89338557; PMID:2503389

A;Accession: S13703

A;Species: preimmune

A;Molecule type: mRNA

A;Residues: 1-103 <PEN>

A;Cross-references: EMBL:X53356; MIM:955310; PID:CAA37442.1; PID:9930227

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetrabramer; immunoglobulin

F;1e-90/Domain: immunoglobulin homology <IMM>

Query Match Similarity 78.2%; Score 440; DB 2; Length 103;

Best Local Similarity 83.3%; Pred. No. 1.3e-30; Mismatches 14; Indels 0; Gaps 0;

Matches 85; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Db 1 DIKMTQSPSMSVSLDVTIPCRASQDQIVVWFOQPKGSKPRTLYLADGVPS 60
 Qy 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 102
 Db 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 102

Query Match Similarity 73.2%; Score 412; DB 2; Length 129;

Best Local Similarity 72.9%; Pred. No. 3.7e-28; Mismatches 18; Indels 0; Gaps 0;

Matches 78; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Db 23 DIKMTQSPSMSVSLDVTIPCRASQDQIVVWFOQPKGSKPRTLYLADGVPS 82
 Qy 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 107
 Db 83 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 129

Query Match Similarity 88.6%; Score 499; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.4e-35; Mismatches 0; Indels 0; Gaps 0;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Db 21 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Qy 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 104
 Db 81 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 104

RESULT 9
 S13703 Ig kappa chain V region (hybridoma NC17-D8) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C;Accession: S13703

R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

Eur. J. Immunol. 19, 1289-1295, 1989

A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clonal selection

A;Reference number: S13685; MUID:89338557; PMID:2503389

A;Accession: S13703

A;Species: preimmune

A;Molecule type: mRNA

A;Residues: 1-103 <PEN>

A;Cross-references: EMBL:X53356; MIM:955310; PID:CAA37442.1; PID:9930227

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetrabramer; immunoglobulin

F;1e-90/Domain: immunoglobulin homology <IMM>

Query Match Similarity 78.2%; Score 440; DB 2; Length 103;

Best Local Similarity 83.3%; Pred. No. 1.3e-30; Mismatches 14; Indels 0; Gaps 0;

Matches 85; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Db 1 DIKMTQSPSMSVSLDVTIPCRASQDQIVVWFOQPKGSKPRTLYLADGVPS 60
 Qy 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 102
 Db 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 102

Query Match Similarity 73.2%; Score 412; DB 2; Length 129;

Best Local Similarity 72.9%; Pred. No. 3.7e-28; Mismatches 18; Indels 0; Gaps 0;

Matches 78; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Db 23 DIKMTQSPSMSVSLDVTIPCRASQDQIVVWFOQPKGSKPRTLYLADGVPS 82
 Qy 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 107
 Db 83 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 129

RESULT 10
 B23986 Ig kappa chain precursor V region (IR2) - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 21-Jan-2000
 C;Accession: B23986
 R;Hellman, L.; Engstrom, A.; Bennich, H.; Pettersson, U.
 Gene 40, 107-114, 1985
 A;Title: Structure and expression of kappa-chain genes in two IgE-producing rat immunocytomas
 A;Reference number: A91541; MUID:86137406; PMID:300517
 A;Accession: B23986
 A;Species: Rattus norvegicus
 A;Molecule type: mRNA
 A;Residues: 1-129 <HEL>
 C;Keywords: heterotetrabramer; immunoglobulin
 F;38-112/Domain: immunoglobulin homology <IMM>

Query Match Similarity 73.2%; Score 412; DB 2; Length 129;

Best Local Similarity 72.9%; Pred. No. 3.7e-28; Mismatches 18; Indels 0; Gaps 0;

Matches 78; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Db 23 DIKMTQSPSMSVSLDVTIPCRASQDQIVVWFOQPKGSKPRTLYLADGVPS 82
 Qy 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 107
 Db 83 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 129

RESULT 10
 B23986 Ig kappa chain precursor V region (IR2) - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 21-Jan-2000
 C;Accession: B23986
 R;Hellman, L.; Engstrom, A.; Bennich, H.; Pettersson, U.
 Gene 40, 107-114, 1985
 A;Title: Structure and expression of kappa-chain genes in two IgE-producing rat immunocytomas
 A;Reference number: A91541; MUID:86137406; PMID:300517
 A;Accession: B23986
 A;Species: Rattus norvegicus
 A;Molecule type: mRNA
 A;Residues: 1-129 <HEL>
 C;Keywords: heterotetrabramer; immunoglobulin
 F;38-112/Domain: immunoglobulin homology <IMM>

Query Match Similarity 73.2%; Score 412; DB 2; Length 129;

Best Local Similarity 72.9%; Pred. No. 3.7e-28; Mismatches 18; Indels 0; Gaps 0;

Matches 78; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSMSYASIGERVTITCKASQDINSYLSWFQPKGSKPRTLYRANRLVDGPS 60
 Db 23 DIKMTQSPSMSVSLDVTIPCRASQDQIVVWFOQPKGSKPRTLYLADGVPS 82
 Qy 61 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 107
 Db 83 RFSGSGSGQDYSLTSLEVEDMGIYCYCLQYDERPYTFCGGTKL 129

RESULT 11
 S13701
 Ig kappa chain V region (hybridoma NC19-E11) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: S13701
 R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
 Eur. J. Immunol. 19, 1281-1285, 1989
 A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clonal selection
 A;Reference number: S13685; MUID:89338557; PMID:2503389
 A;Accession: S13701
 A;Status: preliminary
 A;Residues: 1-101 <PEN>
 A;Cross-references: EMBL:X53154
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin

Query Match 72.8%; Score 410; DB 2; Length 101;
 Best Local Similarity 80.2%; Pred. No. 4.3e-28;
 Matches 81; Conservative 2; Mismatches 18; Indels 0; Gaps 0;
 QY 1 DIKMTQSPSPNSVASYGERVTICKASQDINSVLSWFFQKRGKSRTLYRANLVLGVPS 60
 Db 1 DIRMQSPSSVASYASIGERVITCKASQDIKSYLSWVQKEWKSPTKLIYATSLADGVPS 60
 QY 61 RPFGSGSGDYSLTISLSEYEDMGIVYCYLODESPYTRGG 101
 Db 61 RPFGSGSGDXDYLTTISLESDDATAKXCKXKGESPYTFCGG 101

RESULT 12
 S52789
 Ig kappa chain V region - human (fragment)
 C;Species: Homo sapiens (man)
 C;Accession: S52789
 C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 R;Rocca, A.; Khamlichchi, A.A.; Touchard, G.; Mongenot, B.; Ronco, P.; Denoroy, L.; Deret, A.; Description: Light chain V region gene usage restriction and peculiarities in myeloma; Reference number: S52789
 A;Accession: S52789
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-129 <ROC>
 A;Cross-references: EMBL:X85995; MUID:9758588; PIDN:CAA59987_1; PID:g758589
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 72.8%; Score 410; DB 2; Length 129;
 Best Local Similarity 71.0%; Pred. No. 5.4e-28;
 Matches 76; Conservative 16; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DIKMTQSPSPNSVASYGERVTICKASQDINSVLSWFFQKRGKSRTLYRANLVLGVPS 60
 Db 23 DQMTQSPSSVASYASIGERVITCKASQDINSVLSWVQKEWKSPTKLIYATSLADGVPS 82
 QY 61 RPFGSGSGDYSLTISLSEYEDMGIVYCYLODESPYTRGGKLEIK 107
 Db 83 RFSGSGSGDXDYLTTISLESDDATAKXCKXKGESPYTFCGG 129

RESULT 13
 A4966
 Ig heavy chain V region (PRB-9) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: A4966
 C;Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 23-Jul-1999
 R;Gaton, A.J.; Koprowski, H.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6450-6454, 1990
 A;Title: Influenza virus hemagglutinin-specific antibodies isolated from a combinatorial

A;Koreference number: AJ34956; MUID:90349634; PMID:1696733

A;Accession: AJ34956
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-75 <CAT>

C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 70.9%; Score 399; DB 2; Length 75;
Best Local Similarity 97.3%; Pred. No. 2; -E-27; 0; Mismatches 2; Indels 0; Gaps 0; Matches 73; Conservative 2; MisMatches 0; Indels 0; Gaps 0;

QY 3.0 NSYLSWFOOKPKGSKSPKTLIYRANRLVNDGVPSPRSFSGSGSCDYSLTISSLEYEDMGIVYCL 89
Db 1 NSYLSWFOOKPKGSKSPKTLIYRANRLVNDGVPSPRSFSGSGSCDYSLTISSLEYEDMGIVYCL 60

QY 90 QYDPRPYTGGGTKL 104
Db 61 QYDPRPYTGGGTKL 75

RESULT 14

S36264 Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)

C;Species: Homo sapiens (man)

C;Accession: S36264

R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; EMBL J. 12, 725-734, 1993

A;Title: Human anti-self antibodies with high specificity from phage display libraries

A;Reference number: S36256; MUID:93178448; PMID:7679990

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-107 <GRI>

A;Cross-references: EMBL:Z18845; NID:933426; PIDN:CAA79297.1; PID:9939919

C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM> F.16-90/Domain: immunoglobulin homology

Query Match 70.5%; Score 397; DB 2; Length 107;
Best Local Similarity 68.2%; Pred. No. 5; -E-27; 0; Mismatches 73; Conservative 17; MisMatches 17; Indels 0; Gaps 0; Matches 73; Conservative 17; MisMatches 17; Indels 0; Gaps 0;

QY 1 DIKMTQPSSSMVSAGLGERVTICKASAPDINSYLSWFOOKPKGSKSPKTLIYRANRLVNDGVPSP 60
Db 1 EIVITQPSSSLASAVGIDRVITCRASOSISSYLYWVQOKPKGKAPKLIVAYASSLQSGVPS 60

QY 61 RSGSGSGSQQDYSITISSELEYEDMGIVYCLQXBPFPYTFGGGTKEIK 107
Db 61 RFGSGSGSTNDFTLUTISLQQPDEPATYYCQQVSNYPLTFGGSTKUDIK 107

RESULT 15

S40369 Ig kappa chain - human

C;Species: Homo sapiens (man)

C;Accession: S40369

R;Klein, R.; Jaenichen, R.; Zuchau, H.G.

Bur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Accession: S40312; MUID:94080891; PMID:8258341

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-129 <KLR>

A;Cross-references: EMBL:X72479; NID:g41426; PIDN:CAA51147.1; PID:g41427

C;Superfamily: Immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F.37-11/Domain: immunoglobulin homology <IMM>

Mon Jan 3 13:38:51 2005

us-10-774-076-3.rpr

Page 5

	Query	Match	Score	DB	Length	129;
Best Local Similarity	69.2%	Pred.	No.	6.8e-27		
Matches	74;	Conservative	17;	Mismatches	16;	Indels
Oy	1 DIKMTQSPPSMYASIGERVTICKASQDINSYLSWFOOKPGKSKTLIYRANRLDGVS	60				
Db	22 DQMTQSPSSLSAVGDRVITCRAHVISNLWFMQOKEGKAPRKLIAASSLQSGVPS	81				
Oy	61 RSGSGSGSODPYSUTISLEEDMGTYYCQLDEPFYPTFEGGTKEIK 107					
Db	82 KPSGSQSGSDNDFLTTSISQPEDFATYYCQOYNSTPYTSGQGTKEIK 128					

Search completed: December 29, 2004, 18:06:56
Job time : 15.8437 secs

THIS PAGE IS BLACK (GHOSTED)

Copyright GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 18:05:34 ; Search time 61.8643 Seconds
 (without alignments)
 622.182 Million cell updates/sec

Title: US-10-774-076-3

Perfect score: 563

Sequence: 1 DIKMTQSPSSMYASIGERVITCKASQDINSYLSWFOOKPKGSKPDTLYRANRLVGDPS 60

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 35972771 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA,*

1: /cgm2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgm2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /cgm2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /cgm2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgm2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgm2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgm2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgm2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgm2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgm2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

11: /cgm2_6/ptodata/2/pubpaa/US09_NNEW_PUB.pep:*

12: /cgm2_6/ptodata/2/pubpaa/US09_NNEW_PUB.pep:*

13: /cgm2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

14: /cgm2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

15: /cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgm2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

17: /cgm2_6/ptodata/2/pubpaa/US10_NNEW_PUB.pep:*

18: /cgm2_6/ptodata/2/pubpaa/US11_NNEW_PUB.pep:*

19: /cgm2_6/ptodata/2/pubpaa/US60_NNEW_PUB.pep:*

20: /cgm2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	563	100.0	107	Sequence 3, Appli
2	563	100.0	127	Sequence 11, Appli
3	556	98.8	107	Sequence 33, Appli
4	556	98.8	107	Sequence 1, Appli
5	541	96.1	107	Sequence 26, Appli
6	541	96.1	107	Sequence 26, Appli
7	531	94.3	107	Sequence 123, Appli
8	527	93.6	107	Sequence 21, Appli
9	522	92.7	142	Sequence 2, Appli
10	522	92.7	142	Sequence 4, Appli
11	522	92.7	142	Sequence 4, Appli
12	522	92.7	142	Sequence 4, Appli
13	508	90.2	107	Sequence 27, Appli

RESULT 1

; Sequence 3, Application US/10774076-3

; Publication No. US20040210040A1

; GENERAL INFORMATION:

; APPLICANT: Protein Design Labs, Inc.

; APPLICANT: Landolfi, et al.

; TITLE OF INVENTION: Amipiroglin Antibodies and Their Use to Treat Cancer and Title of Invention: Psoriasis

; FILE REFERENCE: 05882.0064.INPUS01

; CURRENT APPLICATION NUMBER: US/10/774-076

; CURRENT FILING DATE: 2004-02-06

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 3

; LENGTH: 107

; TYPE: PRT

; ORGANISM: mus sp.

; US-10-774-076-3

Query Match Best Local Similarity 100.0%; Score 563; DB 17; Length 107; Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASIGERVITCKASQDINSYLSWFOOKPKGSKPDTLYRANRLVGDPS 60

Db 1 DIKMTQSPSSMYASIGERVITCKASQDINSYLSWFOOKPKGSKPDTLYRANRLVGDPS 60

QY 61 RFSGSGSGDYSLSIJSLSIISYEDMGIVYCLQYBPFYFGGTLEIK 107

Db 61 RFSGSGSGDYSLSIJSLSIISYEDMGIVYCLQYBPFYFGGTLEIK 107

RESULT 2

; Sequence 11, Application US/10774076-3

```

; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphotirequinin Antibodies and Their Use to Treat Cancer and
; FILE REFERENCE: 0582.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 11
; LENGTH: 127
; TYPE: PRT
; ORGANISM: mus sp.
; US-10-774-076-11

Query Match 100.0%; Score 563; DB 17; Length 127;
Best Local Similarity 100.0%; Pred. No. 7.2e-42; Mismatches 0; Indels 0; Gaps 0;
Matches 107; Conservative 0; MisMatch 0; Del 0; Insert 0;

Qy 1 DIKMTQSPSSMVASGERVTICKASQDINSYLSWFOQKCKSKPTLIVANRLVDGPS
Db 21 RFSQSGSGQDYSLTISLEVEDMGIVYCLQDEFPYFEGGTLEIK 107
Qy 61 RFSQSGSGQDYSLTISLEVEDMGIVYCLQDEFPYFEGGTLEIK 107
Db 81 RFSQSGSGQDYSLTISLEVEDMGIVYCLQDEFPYFEGGTLEIK 127
RESULT 3
US-10-436-782-33
; Sequence 33, Application US/10436782
; Publication No. US20040028685A1
GENERAL INFORMATION:
APPLICANT: Kinch, Michael
APPLICANT: Carles-Kinch, Kelly
APPLICANT: Kienmer, Peter
APPLICANT: Langermann, Solomon
TITLE OF INVENTION: EpHA2 Monoclonal Antibodies and Methods of Use Thereof
FILE REFERENCE: 10271-097
CURRENT APPLICATION NUMBER: US/10/436,782
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/379,322
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/418,213
PRIOR FILING DATE: 2002-10-14
PRIOR APPLICATION NUMBER: 60/418,213
PRIOR FILING DATE: 2003-04-03
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 33
LENGTH: 107
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-436-783-1
; Sequence 33, Application US/10436782
; Publication No. US20040028685A1
GENERAL INFORMATION:
APPLICANT: Kinch, Michael
APPLICANT: Carles-Kinch, Kelly
APPLICANT: Kienmer, Peter
APPLICANT: Langermann, Solomon
TITLE OF INVENTION: EpHA2 Monoclonal Antibodies and Methods of Use Thereof
FILE REFERENCE: 10271-097
CURRENT APPLICATION NUMBER: US/10/436,782
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/379,322
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/418,213
PRIOR FILING DATE: 2002-10-14
PRIOR APPLICATION NUMBER: 60/418,213
PRIOR FILING DATE: 2003-04-03
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 1
LENGTH: 107
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-436-783-1
; Sequence 33, Application US/10436782
; Publication No. US20040028685A1
GENERAL INFORMATION:
APPLICANT: Kinch, Michael
APPLICANT: Carles-Kinch, Kelly
APPLICANT: Kienmer, Peter
APPLICANT: Langermann, Solomon
TITLE OF INVENTION: EpHA2 Monoclonal Antibodies and Methods of Use Thereof
FILE REFERENCE: 10271-097
CURRENT APPLICATION NUMBER: US/10/436,782
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/379,322
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/418,213
PRIOR FILING DATE: 2002-10-14
PRIOR APPLICATION NUMBER: 60/418,213
PRIOR FILING DATE: 2003-04-03
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 1
LENGTH: 107
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-340-189-26
; Sequence 26, Application US/10340189
; Publication No. US20030229207A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 W. Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #11.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/340,189
FILING DATE: 10-Jan-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/245,202A
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-Jun-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-Dec-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-Dec-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2
TELECOMMUNICATION INFORMATION:
RESULT 4
US-10-436-783-1
; Sequence 1, Application US/10436783

```

TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-10-340-189-26

Query Match 96.1%; Score 541; DB 14; Length 107;
 Best Local Similarity 96.3%; Pred. No. 5.1e-40;
 Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Query Match 96.1%; Score 541; DB 14; Length 107;
 Best Local Similarity 96.3%; Pred. No. 5.1e-40;
 Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIKMTQSPPSSMYSASIGERVTITCKASODINSYLSWFQQPKGKSPKTLIYRANRLVDGVPs 60
 Db 1 DIKMTQSPPSSMYSASIGERVTITCKASODINSYLSWFQQPKGKSPKTLIYRANRLVDGVPs 60

Qy 61 RFSGSGGSDYSLTISASYEEDMGIVKCYQDYPFPYFGGTKEIK 107
 Db 61 RFSGSGGSDYSLTISASYEEDMGIVKCYQDYPFPYFGGTKEIK 107

Db 61 RFSGSGGSDYSLTISASYEEDMGIVKCYQDYPFPYFGGTKEIK 107

RESULT 6
 US-10-325-696-26
 Sequence 26, Application US/10325696
 Publication No. US20040005630A1
 GENERAL INFORMATION:
 APPLICANT: Scudnicka, Gary M.
 TITLE OF INVENTION: Modified Antibody Variable Domains
 NUMBER OF SEQUENCES: 67
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th Floor
 CITY: Chicago
 STATE: IL
 COUNTRY: United States of America
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/325,696
 FILING DATE: 18-Dec-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/097,980
 FILING DATE: 16-JUN-1998
 APPLICATION NUMBER: 08/107,669
 FILING DATE: 13-AUG-1993
 APPLICATION NUMBER: PCT/US92/110906
 FILING DATE: 14-DEC-1992
 APPLICATION NUMBER: US 07/808,464
 FILING DATE: 13-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Janet M. McNicholas, Ph.D.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 123:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPR: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 123:
 US-10-127-890-123

Query Match 96.1%; Score 541; DB 15; Length 107;
 Best Local Similarity 96.3%; Pred. No. 5.1e-40;
 Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Query Match 96.1%; Score 541; DB 15; Length 107;
 Best Local Similarity 96.3%; Pred. No. 5.1e-40;
 Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIKMTQSPPSSMYSASIGERVTITCKASODINSYLSWFQQPKGKSPKTLIYRANRLVDGVPs 60
 Db 1 DIKMTQSPPSSMYSASIGERVTITCKASODINSYLSWFQQPKGKSPKTLIYRANRLVDGVPs 60

Qy 61 RFSGSGGSDYSLTISASYEEDMGIVKCYQDYPFPYFGGTKEIK 107
 Db 61 RFSGSGGSDYSLTISASYEEDMGIVKCYQDYPFPYFGGTKEIK 107

RESULT 7
 US-10-127-890-123
 Sequence 123, Application US/10127890
 Publication No. US20030161961
 GENERAL INFORMATION:
 APPLICANT: Carroll, Stephen F.
 Scudnicka, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/127,890
 FILING DATE: 23-Apr-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/446,360
 FILING DATE: 13-MAY-1996
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 APPLICATION NUMBER: US 08/164,691
 FILING DATE: 12-MAY-1993
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 APPLICATION NUMBER: US 07/501,707
 FILING DATE: 19-JUN-1992
 APPLICATION NUMBER: US 07/887,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 123:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPR: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 123:
 US-10-127-890-123

Query Match 94.3%; Score 531; DB 14; Length 107;

Best Local Similarity 94.4%; Pred. No. 3.9e-39; Mismatches 2; Indels 0; Gaps 0;

Qy

Db

RESULT 8
US-09-158-120A-21
Sequence 21, Application US/09158120A
Patent No. US20020102257A1
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
Foon, Kenneth A.
Koller, Heinz
TITLE OF INVENTION: MORINE ANTI-IDIOTYPE ANTIBODY 3H1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/797,481
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 09/361,772
FILING DATE: 27-JUL-1999
APPLICATION NUMBER: US 08/579,940
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/365,484
FILING DATE: 28-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-797-481-2

Query Match 93.6%; Score 527; DB 9; Length 107;

Best Local Similarity 92.5%; Pred. No. 8.7e-39; Mismatches 99; Conservative 5; Indels 3; Gaps 0;

Matches 98; Sequence 4, Application US/09044736

Patent No. US20020011872A1

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

Foon, Kenneth A.

Chatterjee, Sunil K.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CELL ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEES: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/844,736

FILING DATE: 09-Apr-1997

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 09/844,736

FILING DATE: April 27, 2001

APPLICATION NUMBER: US 08/838,692

FILING DATE: April 9, 1997

APPLICATION NUMBER: US 60/044,455

FILING DATE: April 12, 1996

APPLICATION NUMBER: US 08/631,085

FILING DATE: April 12, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Polizzi, Catherine M.

REGISTRATION NUMBER: 40,130

REFERENCE/DOCKET NUMBER: 30414-20004.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 142 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-844-736-4

Query Match Score 522; DB 9; Length 142;

Best Local Similarity 91.6%; Pred. No. 3.2e-38; 4;

Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIKMQSPSSMMASIGERVITCKASQDINSVLSWFOQKPGKSKRTLIVRNRLVDGVPS 60

Db 21 DIKMQSPSSMMASIGERVITCKASQDINSVLSWFOQKPGKSKRTLIVRNRLVDGVPS 80

RESULT 12

US-10-162-396-4

Sequence 4, Application US/10162396

Publication No. US20030077274A1

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Chatterjee, Malaya

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Morrison & Foerster

APPLICATION NUMBER: US/10/162,396

FILING DATE: 31-Jul-2002

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 09/844,736

FILING DATE: April 27, 2001

APPLICATION NUMBER: US 08/838,692

FILING DATE: April 9, 1997

APPLICATION NUMBER: US 60/044,455

FILING DATE: April 12, 1996

APPLICATION NUMBER: US 08/631,085

FILING DATE: April 12, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Polizzi, Catherine M.

REFERENCE/DOCKET NUMBER: 30414-2000402

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 142 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-162-396-4

Query Match Score 522; DB 9; Length 142;

Best Local Similarity 91.6%; Pred. No. 3.2e-38; 4;

Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIKMQSPSSMMASIGERVITCKASQDINSVLSWFOQKPGKSKRTLIVRNRLVDGVPS 60

Db 21 DIKMQSPSSMMASIGERVITCKASQDINSVLSWFOQKPGKSKRTLIVRNRLVDGVPS 80

RESULT 12

US-10-819-493-4

Sequence 4, Application US/1019493

Publication No. US20040253230A1

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Chatterjee, Malaya

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Chatterjee, Malaya

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Chatterjee, Malaya

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Chatterjee, Malaya

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Chatterjee, Malaya

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Chatterjee, Malaya

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Chatterjee, Malaya

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Chatterjee, Malaya

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Chatterjee, Malaya

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

APPLICANT: Chatterjee, Malaya

Chatterjee, Sunil K.

Foon, Kenneth A.

TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF

CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1

NUMBER OF SEQUENCES: 6

FILING DATE: April 27, 2001
 APPLICATION NUMBER: US 08/838,692
 FILING DATE: April 9, 1997
 APPLICATION NUMBER: US 60/044,455
 FILING DATE: April 12, 1996
 APPLICATION NUMBER: US 08/631,085
 FILING DATE: April 12, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Jacobson, Jill
 REGISTRATION NUMBER: 40,030
 REFERENCE/DOCKET NUMBER: 304142000403
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 70141
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 SEQUENCE TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-819-493-4

Query Match 92.7%; Score 522; DB 17; Length 142;
 Best Local Similarity 91.6%; Pred. No. 3.2e-38;
 Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMSASLGIVRVTITCKASQDINSYLISWFOQKPGKSPKTLTYRANRLVDGVPs 60
 Db 21 DIKMTQSPSSMSASLGIVRVTITCKASQDINSYLISWFOQKPGKSPKTLTYRANRLVDGVPs 80
 QY 61 RFSGGSGGQDYSLTISLEVDGMGIVYCYQQYDEPYTGFGLK 107
 Db 81 RFSGGSGGQDYSLTISLEVDGMGIVYCYQQYDEPYTGFGLK 127

RESULT 13
 US-10-340-189-27
 ; Sequence 27, Application US/10340189
 ; Publication No. US20030229207A1
 ; GENERAL INFORMATION:
 APPLICANT: Studnicka, Gary M.
 TITLE OF INVENTION: Modified Antibody Variable Domains
 NUMBER OF SEQUENCES: 67
 CORRESPONDENCE ADDRESS:
 ADDRESS: McAndrews, Held & Malloy, Ltd.
 STREET: 500 W. Madison Street, 34th Floor
 CITY: Chicago
 STATE: IL
 COUNTRY: United States of America
 ZIP: 60661

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 SOFTWARE: Patentin Release #1.0, Version #1.25
 APPLICATION NUMBER: US/10/340,189
 FILING DATE: 10-Jan-2003
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/245,202A
 FILING DATE: <Unknown>
 APPLICATION NUMBER: 08/838,692
 FILING DATE: 23-JUN-1993
 APPLICATION NUMBER: PCT/US92/10906
 FILING DATE: 14-DEC-1992
 APPLICATION NUMBER: PCT/US92/10906
 FILING DATE: 14-DEC-1992
 APPLICATION NUMBER: US 07/808,464
 FILING DATE: 13-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9050
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 US-10-340-189-27

Query Match 90.2%; Score 508; DB 14; Length 107;
 Best Local Similarity 89.7%; Pred. No. 4e-37;
 Matches 96; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMSASLGIVRVTITCKASQDINSYLISWFOQKPGKSPKTLTYRANRLVDGVPs 60
 Db 1 DIKMTQSPSSMSASLGIVRVTITCKASQDINSYLISWFOQKPGKSPKTLTYRANRLVDGVPs 60
 QY 61 RFSGGSGGQDYSLTISLEVDGMGIVYCYQQYDEPYTGFGLK 107
 Db 61 RFSGGSGGQDYSLTISLEVDGMGIVYCYQQYDEPYTGFGLK 107

RESULT 14
 US-10-325-696-27
 ; Sequence 27, Application US/10325696
 ; Publication No. US2004005630A1
 ; GENERAL INFORMATION:
 APPLICANT: Studnicka, Gary M.
 TITLE OF INVENTION: Modified Antibody Variable Domains
 NUMBER OF SEQUENCES: 67
 CORRESPONDENCE ADDRESS:
 ADDRESS: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th Floor
 CITY: Chicago
 STATE: IL
 COUNTRY: United States of America
 ZIP: 60661

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 SOFTWARE: Patentin Release #1.0, Version #1.25
 APPLICATION NUMBER: US/10/325,696
 FILING DATE: 18-Dec-2002
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/097,980
 FILING DATE: 16-JUN-1998
 APPLICATION NUMBER: 08/107,669
 FILING DATE: 13-AUG-1993
 APPLICATION NUMBER: PCT/US92/10906
 FILING DATE: 14-DEC-1992
 APPLICATION NUMBER: US 07/808,464
 FILING DATE: 13-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Janet M. McNicholas, Ph.D.
 REGISTRATION NUMBER: 32,918
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9050
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

;US-10-325-696-27
SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Query Match 90.2%; Score 508; DB 15; Length 107;
Best Local Similarity 89.7%; Pred. No. 4e-37;
Matches 96; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
Ov 1 DIKMTQSSSSMAYASILGERVITCKASQDINSYLSWFQOKPGKSPKTLYRANRLVDGVPs 60
Db 1 DIQMTQSSSSMSASILGDRVITCKASQDINSYLSWFQOKPGKSPKTLYRANRLVDGVPs 60
Ov 61 RFGSGSGCQDYSLTJSIISRYEDMGIVYCYCQYDPRPYTGGTKEIK 107
Db 61 RFGSGSGCQDYSLTJSIISRYEDMGIVYCYCQYDPRPYTGGTKEIK 107

RESULT 15
US-10-774-076-14
Sequence 14, Application US/10774076

; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landoll, et al.
; TITLE OF INVENTION: Amfipiregulin Antibodies and Their Use to Treat Cancer and
; Title of Invention: PeoriaB
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-10-774-076-14

Query Match 89.3%; Score 503; DB 17; Length 107;
Best Local Similarity 87.9%; Pred. No. 1.e-36;
Matches 94; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
Ov 1 DIKMTQSSSSMAYASILGERVITCKASQDINSYLSWFQOKPGKSPKTLYRANRLVDGVPs 60
Db 1 DIQMTQSSSSMSASILGDRVITCKASQDINSYLSWFQOKPGKSPKTLYRANRLVDGVPs 60
Ov 61 RFGSGSGCQDYSLTJSIISRYEDMGIVYCYCQYDPRPYTGGTKEIK 107
Db 61 RFGSGSGCQDYSLTJSIISRYEDMGIVYCYCQYDPRPYTGGTKEIK 107

Search completed: December 29, 2004, 18:41:57
Job time : 64.8643 secs

THIS PAGE BLANK (reverse)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 18:05:34 ; Search time 68.8024 Seconds

(without alignments)
622.182 Million cell updates/sec

Title: US-10-774-076-2
Perfect score: 648
Sequence: 1 BIQDQSGPBLVKPGASVKGKSVKRSAGVYAFPTNNYWWKQSHGKSLWMTGIGYIDYYGGGY 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA,*

Minimum Match 100%
Maximum Match 100%
List first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description	RESULT 1	Query	Match Best Local Similarity	Score 100.0%; Pred. No. 2,7e-52;	DB 17; length 119; Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 2, Appli
1	648	100.0	119	17 US-10-774-076-2	Sequence 2, Appli	Qy	1 BIQDQSGPBLVKPGASVKGKSVKRSAGVYAFPTNNYWWKQSHGKSLWMTGIGYIDYYGGGY	60	Sequence 2, Appli	
2	648	100.0	138	17 US-10-774-076-9	Sequence 9, Appli	Db	1 BIQDQSGPBLVKPGASVKGKSVKRSAGVYAFPTNNYWWKQSHGKSLWMTGIGYIDYYGGGY	60	Sequence 2, Appli	
3	564	87.0	119	17 US-10-774-076-12	Sequence 12, Appli	Qy	61 SQKPKGKATITVKQSSSTAYMHNLISRSDAVYTCARRGNRPYFPYDNGQGTITVSS	119	Sequence 2, Appli	
4	564	87.0	138	17 US-10-774-076-17	Sequence 17, Appli	Db	61 SQKPKGKATITVKQSSSTAYMHNLISRSDAVYTCARRGNRPYFPYDNGQGTITVSS	119	Sequence 2, Appli	
5	560.5	86.5	118	15 US-10-462-062-139	Sequence 139, Appli	Qy	61 SQKPKGKATITVKQSSSTAYMHNLISRSDAVYTCARRGNRPYFPYDNGQGTITVSS	119	Sequence 2, Appli	
6	560.5	86.5	118	15 US-10-462-062-140	Sequence 140, Appli	Db	61 SQKPKGKATITVKQSSSTAYMHNLISRSDAVYTCARRGNRPYFPYDNGQGTITVSS	119	Sequence 2, Appli	
7	560.5	86.5	137	15 US-10-462-062-153	Sequence 151, Appli	Qy	61 SQKPKGKATITVKQSSSTAYMHNLISRSDAVYTCARRGNRPYFPYDNGQGTITVSS	119	Sequence 2, Appli	
8	560.5	86.5	137	15 US-10-462-062-154	Sequence 154, Appli	Db	61 SQKPKGKATITVKQSSSTAYMHNLISRSDAVYTCARRGNRPYFPYDNGQGTITVSS	119	Sequence 2, Appli	
9	548.5	84.6	120	15 US-10-372-719-2	Sequence 2, Appli	Qy	61 SQKPKGKATITVKQSSSTAYMHNLISRSDAVYTCARRGNRPYFPYDNGQGTITVSS	119	Sequence 2, Appli	
10	529.9	81.6	117	14 US-10-223-880-2	Sequence 2, Appli	Db	61 SQKPKGKATITVKQSSSTAYMHNLISRSDAVYTCARRGNRPYFPYDNGQGTITVSS	119	Sequence 2, Appli	
11	523.5	80.8	139	15 US-10-365-123-28	Sequence 2, Appli	Qy	61 SQKPKGKATITVKQSSSTAYMHNLISRSDAVYTCARRGNRPYFPYDNGQGTITVSS	119	Sequence 2, Appli	
12	517	79.8	117	15 US-10-383-447-4	Sequence 14, Appli	Db	61 SQKPKGKATITVKQSSSTAYMHNLISRSDAVYTCARRGNRPYFPYDNGQGTITVSS	119	Sequence 2, Appli	
13	517	79.8	117	16 US-10-769-612-3	Sequence 3, Appli	Qy	61 SQKPKGKATITVKQSSSTAYMHNLISRSDAVYTCARRGNRPYFPYDNGQGTITVSS	119	Sequence 2, Appli	

RESULT 2

; Sequence 2, Application US/10774076

; Publication No. US20040210040A1

; GENERAL INFORMATION:

; APPLICANT: Protein Design Labs, Inc.

; ATTORNEY: Landolfi, et al.

; TITLE OF INVENTION: Amipirogrel Antibodies and Their Use to Treat Cancer and

; TITLE OF INVENTION: PSORIASIS

; FILE REFERENCE: 05802_0064_INRUS01

; CURRENT APPLICATION NUMBER: US/10-774-076

; CURRENT FILING DATE: 2004-02-06

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 119

; TYPE: PRT

; ORGANISM: mus sp.

US-10-774-076-2

; QUERY TYPE: PRT

; SEQ ID NO: 119

; LENGTH: 119

; ORGANISM: mus sp.

; RESULT 2

; Sequence 2, Application

; Sequence 3, Application

; Sequence 4, Application

; Sequence 5, Application

; Publication No. US004040100401
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 9
; LENGTH: 138
; TYPE: PRT
; ORGANISM: mub sp.
; US-10-774-076-9
; Query Match 100.0%; Score 648; DB 17; Length 138;
; Best Local Similarity 100.0%; Pred. No. 3.1e-52; Mismatches 0; Indels 0; Gaps 0;
; Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 EILOQSGPVELVKPGASVKSCKASGYAFTNMYWQKOSHGSLEWIGYIDPYGPGY 60
; Db 20 EILOQSGPVELVKPGASVKSCKASGYAFTNMYWQKOSHGSLEWIGYIDPYGPGY 79
; QY 61 SQKFKGATLTVDKSSTAYMHLNSLTSSEDAVYCARGRGNFPYFDPYWGQGTITVSS 119
; Db 80 SQKFKGATLTVDKSSTAYMHLNSLTSSEDAVYCARGRGNFPYFDPYWGQGTITVSS 138

RESULT 3
US-10-774-076-12
; Sequence 12, Application US/10774076
; Publication No. US200402100401
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.004.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Version 3.2
; SEQ ID NO 12
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: Humanized antibody
; US-10-774-076-12

Query Match 100.0%; Score 648; DB 17; Length 138;
Best Local Similarity 100.0%; Pred. No. 3.1e-52; Mismatches 0; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EILOQSGPVELVKPGASVKSCKASGYAFTNMYWQKOSHGSLEWIGYIDPYGPGY 60
Db 20 EILOQSGPVELVKPGASVKSCKASGYAFTNMYWQKOSHGSLEWIGYIDPYGPGY 79
QY 61 SQKFKGATLTVDKSSTAYMHLNSLTSSEDAVYCARGRGNFPYFDPYWGQGTITVSS 119
Db 80 SQKFKGATLTVDKSSTAYMHLNSLTSSEDAVYCARGRGNFPYFDPYWGQGTITVSS 138

RESULT 5
US-10-462-062-139
; Sequence 139, Application US/10462062
; Publication No. US004044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; FILE REFERENCE: 053456-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 139
; LENGTH: 118
; TYPE: PRT
; FEATURE:
; ORGANISM: Artificial sequence
; OTHER INFORMATION: Humanized antibody
; US-10-462-062-139

Query Match 87.0%; Score 564; DB 17; Length 119;
Best Local Similarity 84.9%; Pred. No. 1.6e-44;
Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
QY 1 EILOQSGPVELVKPGASVKSCKASGYAFTNMYWQKOSHGSLEWIGYIDPYGPGY 60
Db 1 EVOLVQSGAEVKPGASVKSCKASGYAFTNMYWQKOSHGSLEWIGYIDPYGPGY 60
QY 61 SQKFKGATLTVDKSSTAYMHLNSLTSSEDAVYCARGRGNFPYFDPYWGQGTITVSS 119
Db 61 SQKFKGATLTVDKSSTAYMHLNSLTSSEDAVYCARGRGNFPYFDPYWGQGTITVSS 119
RESULT 4
US-10-774-076-17
; Sequence 17, Application US/10774076
; Publication No. US20040100401
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 17
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
; US-10-774-076-17

Query Match 87.0%; Score 564; DB 17; Length 138;
Best Local Similarity 84.9%; Pred. No. 1.8e-44; Mismatches 9; Indels 0; Gaps 0;
Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
QY 1 EILOQSGPVELVKPGASVKSCKASGYAFTNMYWQKOSHGSLEWIGYIDPYGPGY 60
Db 20 EVOLVQSGAEVKPGASVKSCKASGYAFTNMYWQKOSHGSLEWIGYIDPYGPGY 79
QY 61 SQKFKGATLTVDKSSTAYMHLNSLTSSEDAVYCARGRGNFPYFDPYWGQGTITVSS 119
Db 80 SQKFKGATLTVDKSSTAYMHLNSLTSSEDAVYCARGRGNFPYFDPYWGQGTITVSS 138

RESULT 6
US-10-462-062-140
; Sequence 140, Application US/10462062
; Publication No. US2004004187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH

APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 140
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of
; , OTHER INFORMATION: H chain V region of anti-TF mouse monoclonal antibody ATR-3
; US-10-462-062-140.

Query Match 86.5%; Score 560.5; DB 15; Length 118;
; Best Local Similarity 89.9%; Pred. No. 3.3e-44; 4; Mismatches 7; Indels 1; Gaps 1;
; Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIQIQQSGPSELVKRGASVRSKCRASGIAFPNTNNWVQSHGKSLEWIGYIDPYGDPY 60
; 1 EIQIQQSGPSELVKRGASVRSKCRASGIAFPNTNNWVQSHGKSLEWIGYIDPYGDPY 60
; QY 61 SQKPKGKATLTVDKSSTAYMHNLSTSISDAVYCARRGNFPYFDWYGQGTILTVSS 119
; 61 SQKPKGKATLTVDKSSTAYMHNLSTSISDAVYCARRGNFPYFDWYGQGTILTVSS 119
; Db 61 NQKPKGKATLTVDKSSTAYMHNLSTSISDAVYCARRGE-GYYPDYWGQGTILTVSS 118
; RESULT 7
; US-10-462-062-153
; Sequence 153, Application US/10462062
; Publication No. US2004004187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,052
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 153
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequence: Full-length amino acid
; , OTHER INFORMATION: sequence for H chain V region of anti-TF mouse monoclonal
; , OTHER INFORMATION: antibody ATR-3
; US-10-462-062-154

Query Match 86.5%; Score 560.5; DB 15; Length 137;
; Best Local Similarity 89.9%; Pred. No. 3.3e-44; 4; Mismatches 7; Indels 1; Gaps 1;
; Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIQIQQSGPSELVKRGASVRSKCRASGIAFPNTNNWVQSHGKSLEWIGYIDPYGDPY 60
; 20 EIQIQQSGPSELVKRGASVRSKCRASGIAFPNTNNWVQSHGKSLEWIGYIDPYGDPY 79
; QY 61 SQKPKGKATLTVDKSSTAYMHNLSTSISDAVYCARRGNFPYFDWYGQGTILTVSS 119
; 80 NQKPKGKATLTVDKSSTAYMHNLSTSISDAVYCARRGE-GYYPDYWGQGTILTVSS 137
; RESULT 9
; US-10-372-719-2
; Sequence 2, Application US/10372719
; Publication No. US20040005643A1
; GENERAL INFORMATION:
; APPLICANT: DE SANTIS, RITA
; APPLICANT: ANASTASI, ANNA MARIA
; TITLE OF INVENTION: ANTI-HUMAN TENASCIN MONOCLOINAL ANTIBODY
; FILE REFERENCE: 2818-141
; CURRENT APPLICATION NUMBER: US/10/372,719
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 60/3359,299
; PRIOR FILING DATE: 2002-02-26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 20
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; , OTHER INFORMATION: antibody ATR-2
; US-10-462-062-153

Query Match 86.5%; Score 560.5; DB 15; Length 137;
; Best Local Similarity 89.9%; Pred. No. 3.3e-44; 4; Mismatches 7; Indels 1; Gaps 1;
; Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIQIQQSGPSELVKRGASVRSKCRASGIAFPNTNNWVQSHGKSLEWIGYIDPYGDPY 60
; 20 EIQIQQSGPSELVKRGASVRSKCRASGIAFPNTNNWVQSHGKSLEWIGYIDPYGDPY 79
; QY 61 SQKPKGKATLTVDKSSTAYMHNLSTSISDAVYCARRGNFPYFDWYGQGTILTVSS 119
; 80 NQKPKGKATLTVDKSSTAYMHNLSTSISDAVYCARRGE-GYYPDYWGQGTILTVSS 137
; RESULT 10
; US-10-372-719-2
; Query Match 84.6%; Score 548.5; DB 15; Length 120;
; Best Local Similarity 86.7%; Pred. No. 4.3e-43; 6; Mismatches 9; Indels 1; Gaps 1;
; Matches 104; Conservative 87; 6; Mismatches 9; Indels 1; Gaps 1;
; , OTHER INFORMATION: ST2146 heavy chain variable region protein sequence
; US-10-372-719-2

QY 1 EIQIQQSGPSELVKRGASVRSKCRASGIAFPNTNNWVQSHGKSLEWIGYIDPYGDPY 60

RESULT 10
 US-10-223-880-2
 ; Sequence 2, Application US/10223880
 ; Publication No. US0030152571A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JONAK, ZDENKA
 ; APPLICANT: TAYLOR, KYUNG O.
 ; TITLE OF INVENTION: ANTI-ALPHABETA3 HUMANIZED MONOCLOINAL
 ; TITLE OF INVENTION: ANTIBODIES
 ; FILE REFERENCE: P5062AC1
 CURRENT APPLICATION NUMBER: US/10/223,880
 CURRENT FILING DATE: 2002-08-20
 PRIOR APPLICATION NUMBER: 09/380,910
 PRIOR FILING DATE: 1999-09-10
 PRIOR APPLICATION NUMBER: PCT/US98/04987
 PRIOR FILING DATE: 1998-03-12
 PRIOR FILING DATE: 1997-03-12
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 117
 TYPE: PRT
 ORGANISM: Mus musculus
 US-10-223-880-2

Query Match 81.6%; Score 529; DB 14; Length 117;
 Best Local Similarity 84.3%; Pred. No. 2.76-41;
 Matches 102; Conservative 8; Mismatches 5; Indels 6; Gaps 2;

Qy 1 BIOLQOSGPBLVKPGASVVKUCKASGAYTINNNWIKQSHGSLEWIGYIDPYGGPY 60
 Db 1 BIOLQOSGPBLVKPGASVVKUCKASGAYTINNNWIKQSHGSLEWIGYIDPYGGPY 60

Qy 61 SQKFGKATITVDSSTAYMHNLSSLTEDSAVYCARR--GKFPYFYDYGQGTIVS 118
 Db 61 NQKFGKATITVDSSTAYMHNLSSLTEDSAVYCARQYGSFA---YNGQGTIVS 116

Qy 119 S 119 ;

Db 117 A 117

RESULT 11
 US-10-365-123-28
 ; Sequence 28, Application US/10365123
 ; Publication No. US20040033365A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiner, Christop
 ; APPLICANT: Scott, Andrew
 ; APPLICANT: Burgess, Antony
 ; TITLE OF INVENTION: HUMANIZED GM-CSF ANTIBODIES
 ; FILE REFERENCE: LUD 5729.1
 ; CURRENT APPLICATION NUMBER: US/10/365,123
 ; CURRENT FILING DATE: 2003-02-12
 ; NUMBER OF SEQ ID NOS: 56
 ; SEQ ID NO 28
 LENGTH: 139

Query Match 81.5%; Pred. No. 1e-40; DB 14; Length 117;
 Best Local Similarity 97%; Conservative 10; Mismatches 11; Indels 1; Gaps 1;
 Matches 97; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

Qy 1 EIQLQOSGPBLVKPGASVVKUCKASGAYTINNNWIKQSHGSLEWIGYIDPYGGPY 60
 Db 18 EVQLQOSGPBLVKPGASVVKUCKASGAYTPTDNHMKQSHGSLEWIGYIDPYGGPY 77

Qy 61 SQKFGKATITVDSSTAYMHNLSSLTEDSAVYCARGNFPYFYDYGQGTIVS 119
 Db 78 NQKFGKATITVDSSTAYMHNLSSLTEDSAVYCARRDPF-YDYGQGTIVS 135

RESULT 12
 US-10-383-447-14
 ; Sequence 14, Application US/10383447
 ; Publication No. US0040096392A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bhaskar, Vinay
 ; APPLICANT: de la Calle, Agustin
 ; APPLICANT: Law, Debbie
 ; APPLICANT: Caras, Ingrid
 ; APPLICANT: Ramakrishnan, Vanitha
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Powers, David
 ; TITLE OF INVENTION: Antibodies Against Cancer Antigen TMEPF2 and Uses Thereof
 ; FILE REFERENCE: US882.0138.NPUS00
 ; CURRENT APPLICATION NUMBER: US/10/383,447
 ; CURRENT FILING DATE: 2002-03-07
 ; PRIOR APPLICATION NUMBER: US 6/0/362,837
 ; PRIOR FILING DATE: 2002-03-08
 ; PRIOR APPLICATION NUMBER: US 6/0/463,812
 ; PRIOR FILING DATE: 2002-12-27
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 14
 ; LENGTH: 117
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Heavy chain variable region

Query Match 79.8%; Score 517; DB 15; Length 117;
 Best Local Similarity 82.4%; Pred. No. 3.4e-40;
 Matches 98; Conservative 9; Mismatches 10; Indels 2; Gaps 1;

Qy 1 BIOLQOSGPBLVKPGASVVKUCKASGAYTINNNWIKQSHGSLEWIGYIDPYGGPY 60
 Db 1 BIOLQOSGPBLVKPGASVVKUCKASGAYTPTDNHMKQSHGSLEWIGYIDPYGGPY 60

Qy 61 SQKFGKATITVDSSTAYMHNLSSLTEDSAVYCARGNFPYFYDYGQGTIVS 119
 Db 61 NQKFGKATITVDSSTAYMHNLSSLTEDSAVYCARRDPF-YDYGQGTIVS 117

RESULT 13
 US-10-763-612-3
 ; Sequence 3, Application US/10769612
 ; Publication No. US2004014983A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Law, Debbie
 ; APPLICANT: Gish, Kurt C.
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Culp, Patricia
 ; TITLE OF INVENTION: Compositions Against Cancer Antigen LIV-1 And Uses Thereof
 ; FILE REFERENCE: 05882.0129.CIUS08
 ; CURRENT APPLICATION NUMBER: US/10/769,612
 ; CURRENT FILING DATE: 2004-01-29
 ; PRIOR APPLICATION NUMBER: 60/443,712
 ; PRIOR FILING DATE: 2003-01-29
 ; PRIOR APPLICATION NUMBER: 09/642,034
 ; PRIOR FILING DATE: 2000-08-18

Query Match 80.8%; Score 523.5; DB 15; Length 139;

US-10-365-123-28
 ; OTHER INFORMATION: amino acid sequence for murine 19/2 heavy chain variable region

Query Match 80.8%; Score 523.5; DB 15; Length 139;

```

; PRIOR APPLICATION NUMBER: 09/525,361
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 09/453,137
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 09/450,810
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/268,865
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 3
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-769-612-3

Query Match 79.8%; Score 517; DB 16; Length 117;
Best Local Similarity 82.4%; Pred No. 3; e-40; Mismatches 10; Indels 2; Gaps 1;
Matches 98; Conservative 9; APPLICANT: Soares, M. Melina
Qy 1 EIQLOQSGPBLVKPGASVKSCKASGAYAFNMYWIKOSHGSLEWIGYIDPYGPGY 60
Db 1 BIQLOQSGPBLMKPGASVKSCKASTYSFRYFHWKOSHGSLEWIGYIDPENGGRGY 60
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/642,060
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-642-120-2

Query Match 79.4%; Score 514.5; DB 16; Length 152;
Best Local Similarity 80.0%; Pred. No. 7.7e-40; Mismatches 10; Indels 1; Gaps 1;
Matches 96; Conservative 10; APPLICANT: Thorpe, Philip E.
Qy 1 EIQLOQSGPBLVKPGASVKSCKASGAYAFNMYWIKOSHGSLEWIGYIDPYGPGY 60
Db 20 EVOLQOQSGPBLKPGASVKSCKASGSPFTGYNMWWIKOSHGSLEWIGHIDPYGPGY 79
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/642,120
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-642-120-2

Query Match 79.4%; Score 514.5; DB 16; Length 152;
Best Local Similarity 80.0%; Pred. No. 7.7e-40; Mismatches 10; Indels 1; Gaps 1;
Matches 96; Conservative 10; APPLICANT: Soares, M. Melina
Qy 1 EIQLOQSGPBLVKPGASVKSCKASGAYAFNMYWIKOSHGSLEWIGYIDPYGPGY 60
Db 20 EVOLQOQSGPBLKPGASVKSCKASGSPFTGYNMWWIKOSHGSLEWIGHIDPYGPGY 79
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/642,120
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-642-120-2

RESULT 15
US-10-642-060-2
; Sequence 2, Application US/10642060
; Publication No. US20040131621A1
; GENERAL INFORMATION:
; APPLICANT: Thorpe, Philip E.
; TITLE OF INVENTION: Methods for Treating Viral Infections Using Antibodies to
; TITLE OF INVENTION: Aminophospholipids
; FILE REFERENCE: 4001.002982
; CURRENT APPLICATION NUMBER: US/10/642,060
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/621,269
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-642-120-2

Query Match 79.4%; Score 514.5; DB 16; Length 152;
Best Local Similarity 80.0%; Pred. No. 7.7e-40; Mismatches 10; Indels 1; Gaps 1;
Matches 96; Conservative 10; APPLICANT: Thorpe, Philip E.
Qy 1 EIQLOQSGPBLVKPGASVKSCKASGAYAFNMYWIKOSHGSLEWIGYIDPYGPGY 60
Db 20 EVOLQOQSGPBLKPGASVKSCKASGSPFTGYNMWWIKOSHGSLEWIGHIDPYGPGY 79
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/642,120
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-642-120-2

Query Match 79.4%; Score 514.5; DB 16; Length 152;
Best Local Similarity 80.0%; Pred. No. 7.7e-40; Mismatches 10; Indels 1; Gaps 1;
Matches 96; Conservative 10; APPLICANT: Thorpe, Philip E.
Qy 1 EIQLOQSGPBLVKPGASVKSCKASGAYAFNMYWIKOSHGSLEWIGYIDPYGPGY 60
Db 20 EVOLQOQSGPBLKPGASVKSCKASGSPFTGYNMWWIKOSHGSLEWIGHIDPYGPGY 79
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/642,120
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-642-120-2

Search completed: December 29, 2004, 18:41:54
Job time : 74.8024 Secs

```

THIS PAGE BLANK (USPTO)

and prevention of thrombotic disease, especially of disseminated intravascular coagulation (DIC). The humanised antibody has the high binding activity of the mouse monoclonal antibody but greatly reduced immunogenicity. A4Z33001 to A4Z33091 and Y52707 to AY52767 represent sequences used in the exemplification of the present invention

CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 118 AA;

Query Match 86.5%; Score 560.5; DB 2; Length 118;
 Best Local Similarity 89.9%; Preb. No. 5.7e-40; Mismatches 7;
 Matches 107; Conservative 4; Gaps 1; Identities 1;
 Matches 107; Conservative 4; Gaps 1; Identities 1;

QY	1	EIQQQQSEPBELVREGASVUKSCKASGATNMNNAVKVSKHQSLEWIGIDPYGDPGY	60
		: : : : : : : : : : :	
Db	1	EIQQQQSEPBELVREGASVUKSCKASGATNMNNAVKVSKHQSLEWIGIDPYGDPGY	60
QY	61	SQKRGKAKLTVDKSSSTAPMHNLSITSDSAVYCARGNFPYFDYNGQGTILTVSS	119
	:	: : : : : : : : : : : :	
Db	61	NQKFGKAKLTVDKSSSTAPMHNLSITSDSAVYCARGNFPYFDYNGQGTILTVSS	118

RESULT 2

RAY52756
 ID AAY52756 standard; protein; 118 AA.
 XK
 XX
 AC AAY52756;
 DT 26-JAN-2000 (first entry)
 DE Anti-tissue factor mouse monoclonal antibody ATR-3 H chain v region.
 XX
 KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody; ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC; disseminated intravascular coagulation; immunogenicity; chimeric.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN WO951743-A1.
 XX
 PD 14-OCT-1999.
 XX
 PR 02-APR-1999; 99WO-JP001768.
 XX
 PR 03-APR-1998; 98JP-00091850.
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PT Sato K, Adachi H, Yabuta N;
 XX
 DR WPI; 1999-620204/53.
 DR N-PASB; AA233007.
 XX
 PT Humanised antibody recognizing human tissue factor, used for treatment of disseminated intravascular coagulation.
 XX
 PS Claim 1; Page 275; 291pp; Japanese.

The present invention describes chimeric antibody (Ab) heavy (H) chains containing the variable region of the H chain of a mouse monoclonal Ab recognising human tissue factor (hTF) and the constant region of the H chain of a human Ab. The variable region is one of six specified sequences (which are the H chain variable regions from mouse monoclonal Ab's, ATR-2, 3, 4, 5, 7 or 8). Also described are chimeric Ab light (L) chains containing the variable region of the L chain of a mouse monoclonal Ab recognising human tissue factor (hTF) and the constant region of the L chain of a human Ab, the variable region being one of six specified sequences (which are the L chain variable regions from mouse monoclonal Ab's ATR-2, 3, 4, 5, 7 or 8). The chimeric Ab's can be used for the treatment and prevention of thrombotic disease, especially of disseminated intravascular coagulation (DIC). The humanised antibody has the high hTF binding activity of the mouse monoclonal antibody but greatly reduced immunogenicity, averting adverse side effects such as vascular occlusion.

New anti-human tenascin ST2146 monoclonal antibody, and its proteolytic fragments that bind to an antigenic epitope within the EGF-like repeat of human tenascin C, useful for treating tumors, e. g. gliomas, cystic brain tumors.

Best local similarity 86.7%; Pred. No. 6e-39; 9, Mismatches 1, Indels 1; Gaps 1;
 Matches 104; Conservative 6; Mismatches 9, Indels 1; Gaps 1;

QY	1 BIQHQSGPGLVKGASVVKSCGASVATINMMWVKQSHGKSLIEWIGYIDPYGDEY 60
DB	1 KVKLQGSGLVKGASVVKSCGASVATINMMWVKQSHGKSLIEWIGYIDPYGDEY 60
QY	61 SOKRKGKATITVDKSSSTAYMHLNSLTSETSAVTCARGRGNFPY-FDWGQ3TTLVSS 119
DB	61 NQKEFKGKATITVDKSSSTAYMHLNSLTSETSAVTCARGRGGSIYAMDINGQITVSS 120

RESULT 4

ADC24943

ID

ADC24943

XX

AC

XX

DT

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

QY

DB

XX

AC

XX

DT

XX

DB

XX

CC activities. The GM-CSF nucleic acid is useful for blocking GM-CSF and its CC effects on cells, such as in preventing the development of rheumatoid CC arthritis and other inflammatory diseases and conditions. This sequence CC represents the murine 19/2 heavy chain variable region protein of the CC invention.

SQ Sequence 140 AA;

Query Match 83.5%; Score 541; DB 7; Length 140;
Best Local Similarity 82.4%; Pred. No. 3.1e-38;
Matches 98; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

OY 1 EIQLOQSGPVELYKPGASVVKVSCKASGQAFNTNMWVQSHGSLEWIGYIDPYGDPGV 60
Db 18 EVOLQDQSGPVELYKPGASVVKVSCKASGQAFNTNMWVQSHGSLEWIGYIDPYGDPGV 77
OY 61 SOKFKGKATLTVDKSSSTAYMHINSLTSEDAVYCARRNPNPYFDYNGQGTIVSS 119
Db 78 NQEFKFKATLTVDKSSSTAYMHINSLTSEDAVYCARRNPNPYFDYNGQGTIVSS 136

RESULT 6

AAW95481 ID AAW95481 standard; protein; 116 AA.

AC AAW95481;

XX

DT 29-MAR-1999 (first entry)

XX

DE Mouse derived RT3 phage antibody heavy chain pattern A genetic sequence.

XX Catalytic; antibody; phage display; immunising; phage expression vector; prodrug; scFv.

OS OS sp.

XX

PN US5855885-A.

XX

PD 05-JAN-1999.

KW prodrug; scFv.

XX

PF 14-JUL-1994; 94US-00273146.

OS

XX

PR 22-JAN-1993; 93US-00007684.

XX

PA (MCCA/) MCCAFFERTY J.

PA (CHIS/) CHISWELL D.

PA (DARS/) DARSLEY M J.

PA (TITM/) TITMAS R C.

PA (MART/) MARTIN M T.

PA (KENT/) KENTEN J H.

PA (SMIT/) SMITH R.

PA (FITZ/) FITZGERALD K.

PA (WILL/) WILLIAMS R O.

XX

PT Fitzgerald K, Darstley MJ, Williams RO, Smith R, Martin MT;

XX Kenten JH, Chiswell D, McCafferty J, Titmas RC;

DR WPI; 1999-105036/09.

DR N-PSDB; AAX00880.

XX

PT Production of catalytic antibodies displayed on bacteriophages - comprises generating a gene library of antibody-derived domains inserting coding into a phage expression vector and isolating the catalytic antibodies.

XX

PS Example 4; Fig 12A-J; 117pp; English.

XX The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating a gene library of antibody-derived domains, (b) inserting coding for the domains into a phage expression vector and isolating the catalytic antibodies. The

CC peptide. The catalytic antibodies can be isolated by preparing an

CC antigen; optionally immunising an animal with the antigen; generating a CC library of VH and VL domains from the immunised animal; cloning the VH CC and VL domains into a phage expression vector to generate phage display CC antibodies; selecting phage display antibodies which bind specifically to CC the antigen; screening the selected phage display antibodies for CC catalytic activity to substrate; and isolating the catalytic peptide in CC tandem with a myc peptide. The processes are used to produce catalytic CC antibodies, which can be used for in vivo activation of a prodrug. The present sequence represents a genetic sequence of heavy chain pattern A CC from mouse derived RT3 phage antibodies.

XX Sequence 116 AA;

SQ

Query Match 81.7%; Score 529.5; DB 2; Length 116;
Best Local Similarity 85.7%; Pred. No. 2.4e-37;
Matches 102; Conservative 6; Mismatches 8; Indels 3; Gaps 2;

OY 1 EIQLOQSGPVELYKPGASVVKVSCKASGQAFNTNMWVQSHGSLEWIGYIDPYGDPGV 60
Db 1 QVQLQDQSGPVELYKPGASVVKVSCKASGQAFNTNMWVQSHGSLEWIGYIDPYGDSGY 60

OY 61 SOKFKGKATLTVDKSSSTAYMHINSLTSEDAVYCARRNPNPYFDYNGQGTIVSS 119
Db 61 NQEFKFKATLTVDKSSSTAYMHINSLTSEDAVYCARRNPNPYFDYNGQGTIVSS 136

RESULT 7

ID AAW84033

XX

AC AAW84033;

XX

DT 15-MAR-1999 (first entry)

XX

DB Murine vitronectin alpha- ν beta-3 receptor Mab VH region.

XX

KW Humanised antibody; monoclonal antibody; Mab; antibody engineering;

KW mouse; human; vitronectin; alpha- ν beta-3; receptor; retinoic acid; cancer;

KW metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis; diabetes;

KW diabetic retinopathy; inflammation; macular degeneration; osteoporosis;

KW Paget's disease; hyperparathyroidism; hypercalcemia; therapy;

KW immunotherapy.

XX

OS Mus sp.

XX

PR Key

FT Location/Qualifiers

FT /label= CDR1

FT Region

FT 31-.35

FT /label= CDR2

FT Region

FT 50-.66

FT /label= CDR3

FT 99-.105

FT /label= CDR3

XX

PN W09840488-A1.

XX

PR 17-SEP-1998.

XX

PR 12-MAR-1998; 98WO-US004987.

XX

BR 12-MAR-1997; 97US-0039609P.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Jonak ZL, Johanson KO, Taylor AH;

XX

DR WPI; 1999-034590/03.

XX New anti alpha- ν beta-3 vitronectin receptor antibodies - used for

PT immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory

PT disorders, atherosclerosis, restenosis, cancers or osteoporosis.

XX

Example 13; Page 56; 97pp; English.

XX
CC This is the amino acid sequence of the heavy chain variable region (VH)
CC of the anti-human alpha- ν beta-3 vitronectin receptor murine monoclonal
CC antibody D12, as deduced from isolated cDNA (see AAV71797). D12 VH and VL
(see AAW84094) show sequence similarity to Kabat VH subgroup I (see
CC AAW84095) and Kabat VK subgroup III (see AAW84096), respectively.
CC Humanised VH (see AAW84097) and VL (see AAW84098) were constructed by
CC combining the framework regions of the human V region consensus sequences
CC with complementary determining regions of D12 (keeping some preferred
reactive with the human alpha- ν beta-3 protein receptor and capable of
neutralising the receptor. They can be used for passive immunotherapy of
CC a disorder mediated by the alpha- ν beta-3 receptor, e.g. cardiovascular
disorders or angiogenic-related disorders, such as angiogenesis,
CC associated with diabetic retinopathy, atherosclerosis and restenosis,
CC chronic inflammatory disorders, macular degeneration, rheumatoid
arthritis and cancer, e.g. solid tumour metastasis, and diseases where
CC bone resorption is associated with pathology such as osteoporosis,
CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
CC osteolytic lesions produced by bone metastasis, bone loss due to
CC immobilisation or sex hormone deficiency. They can also be used for
CC targeted drug therapy, and for detection and diagnosis
XX Sequence 117 AA;

Query Match Score 81.6%; Score 529; DB 2; Length 117;
Best Local Similarity 84.3%; Pred. No. 2.6e-37; Matches 102; Conservative 8; Mismatches 5; Indels 6; Gaps 2;
QV 1 EIQLOQSQPELVRGASVVKVSCKASGAYAPINTNYWIKQOSHGSLEWIGYIDPYGPGY 60
Db 1 EIQLOQSQPELVRGASVVKVSCKASGAYAPINTNYWIKQOSHGSLEWIGYIDPYGPGY 60
QY 61 SOKPKGKATLTVDKSSSTAMHNLNLTSEDSAVYCARRGNP-PYVFDYWGQGTLLVSS 118
Db 61 SOKPKGKATLTVDKSSSTAMHNLNLTSEDSAVYCARRGNP-PYVFDYWGQGTLLVSS 118
QV 61 NOKEKGKAITLTVDKSSSTAMHNLNLTSEDSAVYCARRGNP-S---YWGQGTLLVSS 116
Db 117 A 117
XX Sequence 119 AA;

RESULT 8
ABP96759
ID ABP96759 standard; protein; 214 AA.

XX
AC ABP96759;
DT 05-JUN-2003 (first entry)
DB TSH receptor antibody 17D2 heavy chain amino acid sequence.
XX Myotropin receptor; TSH receptor; epitope region; antibody;
KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
KW gene therapy; immune reaction; thyroid cancer.
OS Synthetic.
XX WO2003018632-A2.

XX
PD 06-MAR-2003.
XX 21-AUG-2002; 2002WO-GB003831.
XX 23-AUG-2001; 2001GB-00020649.
PR 01-JUL-2002; 2002GB-00015212.
XX
(RSRR-) RSR LTD.

XX
PI Smith BR, Furmaniak J, Sanders JP;
XX WPI; 2003-290051/28.
DR N-PSDB; ACC44914.

XX
PT New polypeptide sequence having part or all of the primary structural
PT conformation of one or more TSH receptor epitopes, useful for treating an
PT autoimmune disease associated with an immune reaction to a TSH receptor,
e.g. thyroid cancer.

XX
PS Claim 71; FIG 17; 196pp; English.

CC The present invention describes a polypeptide sequence comprising part or
CC all of the primary structural conformation of one or more thyrotropin
CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
CC produced in response to a TSH receptor interact. Also described: (1) one
CC or more receptor TSH epitopes with which the autoantibodies and/or lymphocytes
CC or lymphocytes interact, as with the polypeptide sequence described above;
CC (2) a method of screening for autoantibodies or lymphocytes produced in
CC response to a TSH receptor in a sample of body fluid obtained from a
CC subject suspected of suffering from, susceptible to, having or recovering
CC from autoimmune disease associated with an immune reaction to a TSH
CC receptor; (3) a binding partner for a TSH receptor, which is capable of
CC binding to a TSH receptor to stimulate the TSH receptor, where the
CC binding partner does not comprise TSH or naturally produced antibodies to
the TSH receptor; and (4) a combination comprising the binding partner
and one or more further agents capable of stimulating thyroid tissue,
and/or tissue containing a TSH receptor, for simultaneous, separate or
CC sequential use in stimulating thyroid tissue, and/or tissue containing a
TSH receptor. A TSH receptor has cytostatic activity and can be used in
CC gene therapy. The polypeptide, compositions and methods from the present
invention can be used for treating an autoimmune disease associated with
CC an immune reaction to a TSH receptor. The specific binding partner is
useful for the manufacture of a medicament for stimulating thyroid tissue
or tissue containing a TSH receptor, and for treating thyroid cancer.
AC44874 to ACC4905 and ABP96719 to ABP96750 represent TSH receptor
ACC44874 to ACC4905 and ABP96719 to ABP96750 represent TSH receptor
and VL domains given in ABP96751 to ABP96778, which are used in the
CC exemplification of the present invention
XX Sequence 214 AA;

XX
Query Match Score 81.1%; Score 525.5; DB 6; Length 214;
Best Local Similarity 81.7%; Pred. No. 9.7e-37; Matches 98; Conservative 11; Mismatches 10; Indels 1; Gaps 1;
QY 1 EIQLOQSQPELVRGASVVKVSCKASGAYAPINTNYWIKQOSHGSLEWIGYIDPYGPGY 60
Db 1 DVQILOQSQPELVRGASVYSKCKASGAYAPINTNYWIKQOSHGSLEWIGYIDPYGPGY 60
QY 61 SOKPKGKATLTVDKSSSTAMHNLNLTSEDSAVYCARRGNP-PYVFDYWGQGTLLVSS 119
Db 61 NOKEKGKAITLTVDKSSSTAMHNLNLTSEDSAVYCARRGNP-S---YWGQGTLLVSS 120
XX Sequence 215 AA;

XX
RESULT 9
ABP96760
ID ABP96760 standard; protein; 214 AA.

XX
AC ABP96760;
DT 05-JUN-2003 (first entry)

XX
DB TSH receptor antibody 17D2 heavy chain amino acid sequence.
XX Myotropin receptor; TSH receptor; epitope region; antibody;
KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
KW gene therapy; immune reaction; thyroid cancer.
OS Synthetic.
XX WO2003018632-A2.

XX
PD 06-MAR-2003.
XX 21-AUG-2002; 2002WO-GB003831.
XX 23-AUG-2001; 2001GB-00020649.
PR 01-JUL-2002; 2002GB-00015212.
XX
(RSRR-) RSR LTD.

XX
PI Smith BR, Furmaniak J, Sanders JP;
XX WPI; 2003-290051/28.
DR N-PSDB; ACC44914.

PR XX
PR XX
PR XX
PA PA
XX (RSRR-) RSR LTD.
PI PI
XX DR
XX WPI; 2003-290051/2B.
DR N-PSDB; ACC44915.

PT New polypeptide sequence having part or all of the primary structural conformation of one or more TSH receptor epitopes, useful for treating an autoimmune disease associated with an immune reaction to a TSH receptor, e.g. thyroid cancer.

PT Claim 67; Fig 18; 196pp; English.

CC The present invention describes a polypeptide sequence comprising part or all of the primary structural conformation of one or more thyrotropin (TSH) receptor epitopes with which autoantibodies and/or lymphocytes produced in response to a TSH receptor interact. Also described: (1) one or more TSH receptor epitopes with which the autoantibodies and/or lymphocytes interact, as with the polypeptide sequence described above; (2) a method of screening for autoantibodies or lymphocytes produced in response to a TSH receptor in a sample of body fluid obtained from a subject suspected of suffering from, susceptible to, having or recovering from autoimmune disease associated with an immune reaction to a TSH receptor; (3) a binding partner for a TSH receptor, which is capable of binding to a TSH receptor to stimulate the TSH receptor, where the binding partner does not comprise TSH or naturally produced antibodies to the TSH receptor; and (4) a combination comprising the binding partner and one or more further agents capable of stimulating thyroid tissue, and/or tissue containing a TSH receptor, for simultaneous, separate or sequential use in stimulating thyroid tissue, and/or tissue containing a TSH receptor. A TSH receptor has cytostatic activity and can be used in gene therapy. The polypeptide, compositions and methods from the present invention can be used for treating an autoimmune disease associated with an immune reaction to a TSH receptor. The specific binding partner is useful for the manufacture of a medicament for stimulating thyroid tissue or tissue containing a TSH receptor, and for treating thyroid cancer.

CC ACC44874 to ACC44905 and ABP6719 to ABP6750 represent TSH receptor sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH and VL domains given in ABP96751 to ABP96778, which are used in the exemplification of the present invention

CC Sequence 214 AA;

Query Match 81.1%; Score 525.5; DB 6; Length 214;
Best Local Similarity 81.7%; Pred. No. 9.7e-37;
Matches 98; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

OY 1 EIQLOQSGPGLVKPGASVSKCAGSYAFNTNMMWYKOSHGSLEWGYIDPYGPGY 60
Db 1 DVQIQQSGPGLVKPGASVSKCAGSYAFNTNMMWYKOSHGSLEWGYIDPYGATSY 60

RESULT 10
ABP9673
ID ABP9673 standard; protein; 214 AA.
XX
AC ABP9673;
XX
DT 05-JUN-2003 (first entry)
XX
DE TSH receptor antibody 14D3 heavy chain amino acid sequence.
XX
KW Thyrotropin receptor; TSH receptor; epitope region; antibody;
KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
KW gene therapy; immune reaction; thyroid cancer.

XX OS Synthetic.
XX PN WO2003018632-A2.
XX PD 06-MAR-2003.
XX PF 21-AUG-2002; 2002WO-GB003831.
XX PR 23-AUG-2001; 2001GB-00020649.
PR 01-JUL-2002; 2002GB-00015212.
XX PR (RSRR-) RSR LTD.
XX DR N-PSDB; ACC44915.
XX WPI; 2003-290051/2B.
DR N-PSDB; ACC44915.
XX PT New polypeptide sequence having part or all of the primary structural conformation of one or more TSH receptor epitopes, useful for treating an autoimmune disease associated with an immune reaction to a TSH receptor, e.g. thyroid cancer.

CC The present invention describes a polypeptide sequence comprising part or all of the primary structural conformation of one or more thyrotropin (TSH) receptor epitopes with which autoantibodies and/or lymphocytes produced in response to a TSH receptor interact. Also described: (1) one or more TSH receptor epitopes with which the autoantibodies and/or lymphocytes interact, as with the polypeptide sequence described above; (2) a method of screening for autoantibodies or lymphocytes produced in response to a TSH receptor in a sample of body fluid obtained from a subject suspected of suffering from, susceptible to, having or recovering from autoimmune disease associated with an immune reaction to a TSH receptor; (3) a binding partner for a TSH receptor, which is capable of binding to a TSH receptor to stimulate the TSH receptor, where the binding partner does not comprise TSH or naturally produced antibodies to the TSH receptor; and (4) a combination comprising the binding partner and one or more further agents capable of stimulating thyroid tissue, and/or tissue containing a TSH receptor, for simultaneous, separate or sequential use in stimulating thyroid tissue, and/or tissue containing a TSH receptor. A TSH receptor has cytostatic activity and can be used in gene therapy. The polypeptide, compositions and methods from the present invention can be used for treating an autoimmune disease associated with an immune reaction to a TSH receptor. The specific binding partner is useful for the manufacture of a medicament for stimulating thyroid tissue or tissue containing a TSH receptor, and for treating thyroid cancer.

CC ACC44874 to ACC44905 and ABP6719 to ABP6750 represent TSH receptor sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH and VL domains given in ABP96751 to ABP96778, which are used in the exemplification of the present invention

CC Sequence 214 AA;

Query Match 80.3%; Score 520.5; DB 6; Length 214;
Best Local Similarity 80.0%; Pred. No. 2.6e-36;
Matches 96; Conservative 13; Mismatches 10; Indels 1; Gaps 1;

OY 1 EIQLOQSGPGLVKPGASVSKCAGSYAFNTNMMWYKOSHGSLEWGYIDPYGPGY 60
Db 1 DVQIQQSGPGLVKPGASVSKCAGSYAFNTNMMWYKOSHGSLEWGYIDPYGATSY 60

RESULT 11
ABP9674
ID ABP9674 standard; protein; 214 AA.
XX
AC ABP9674;
XX
DT 05-JUN-2003 (first entry)
XX
DE TSH receptor antibody 14D3 heavy chain amino acid sequence.
XX
KW Thyrotropin receptor; TSH receptor; epitope region; antibody;
KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
KW gene therapy; immune reaction; thyroid cancer.

AC	ABP96764,	QY	61 SOKKGKATLIVDQSSAYMHNLTSRDAVYCARGNF PYFYDWGQSTLTWSS 119
XX		: : : : : : : : : : :	61 NOKFEGKATLIVDQSSAYMHNLTSRDAVYCARGNF PYFYDWGQSTLTWSS 120
DT	05-JUN-2003 (first entry)	ID	ADC79231
XX	TSH receptor antibody 14D3 heavy chain amino acid sequence.	XX	ADC79231 standard; protein; 239 AA.
DB	KW Thyrotropin receptor; TSH receptor; epitope region; antibody; autoantibody; autoimmune disease; thyroid tissue; cytostatic; gene therapy; immune reaction; thyroid cancer.	XX	AC ADC79231;
XX	Synthetic.	XX	DT 01-JAN-2004 (first entry)
PN	WO2003018632-A2.	XX	XX Anti-CA125 scFv's VK-8-1.9 amino acid sequence.
XX		XX	DEB
PD	06-MAR-2003.	XX	XX CA 125 tumour antigen; CA 125 tumour antigen modulator; cytostatic; gene therapy.
XX	21-AUG-2002; 2002WO-GB003831.	XX	CA 125 tumour antigen-associated disease; cytostatic; gene therapy.
PP	PR 23-AUG-2001; 2001GB-00020649.	XX	Synthetic.
XX	01-JUL-2002; 2002GB-00015212.	OS	OS
PA	(RSRR-) RSR LTD.	PN	PN WO2003076465-A2.
XX		XX	XX PD 18-SEP-2003.
PI	Smith BR, Furmaniak J, Sanders JP;	XX	XX PP 11-MAR-2003; 2003WO-CA000341.
XX		XX PR 11-MAR-2002; 2002US-0363306P.	
DR	WPI; 2003-290051/28.	PR 28-FEB-2003; 2003CA-02420494.	
XX	N-PSDB; ACC44919.	PA	PA (IVSH-) UNIV SHERBROOKE.
XX	New polypeptide sequence having part or all of the primary structural conformation of one or more thyrotropin autoimmunity disease associated with an immune reaction to a TSH receptor, e.g. thyroid cancer.	XX	XX DR WPI; 2003-722323/68.
PT	conformation of one or more TSH receptor epitopes, useful for treating an	XX	XX PT New modulator capable of negatively modulating a CA 125 tumor antigen in a mammalian cell, useful for preparing a composition for preventing or treating CA 125 tumor antigen-associated disease in a mammal.
PT	autoimmune disease associated with an immune reaction to a TSH receptor, which is capable of lymphocytes interact, as with the polypeptide sequence described above; e.g. thyroid cancer.	XX	XX PT treating CA 125 tumor antigen-associated disease in a mammal.
XX	Claim 67; Fig 22; 196pp; English.	XX	XX PS Disclosure; Fig 29C; 90pp; English.
CC	The present invention describes a polypeptide sequence comprising part or all of the primary structural conformation of one or more thyrotropin (TSH) receptor epitopes with which autoantibodies and/or lymphocytes produced in response to a TSH receptor interact. Also described: (1) one or more receptor TSH epitopes with which the autoantibodies and/or lymphocytes interact, as with the polypeptide sequence described above; (2) a method of screening for autoantibodies or lymphocytes produced in response to a TSH receptor in a sample of body fluid obtained from a subject suspected of suffering from, susceptible to, having or recovering from autoimmune disease associated with an immune reaction to a TSH receptor; (3) a binding partner for a TSH receptor, which is capable of binding to a TSH receptor to stimulate the TSH receptor, where the binding partner does not comprise TSH or naturally produced antibodies to the TSH receptor; and (4) a combination comprising the binding partner and one or more further agents capable of stimulating thyroid tissue, and/or tissue containing a TSH receptor, for simultaneous separate or sequential use in stimulating thyroid tissue, and/or tissue containing a TSH receptor. A TSH receptor has cytotoxic activity and can be used in gene therapy. The polypeptide, compositions and methods from the present invention can be used for treating an autoimmune disease associated with an immune reaction to a TSH receptor. The specific binding partner is useful for the manufacture of a medicament for stimulating thyroid tissue or tissue containing a TSH receptor, and for treating thyroid tissue	XX	XX CC The present invention describes a modulator capable of negatively modulating a CA 125 tumour antigen in a mammalian cell. Also described: (1) a recombinant nucleic acid comprising at least one sequence selected from the group consisting of ADC79233, ADC79234, ADC79235, ADC79237 and ADC79238; (2) a vector comprising the recombinant nucleic acid; (3) a host cell; (4) a pharmaceutical composition; (5) preventing or treating CA 125 tumour antigen-associated disease in a mammal; and (6) negatively modulating a CA 125 tumour antigen in a mammalian cell. A modulator capable of negatively modulating a CA 125 tumour antigen has cytotoxic activity, and can be used in gene therapy. The modulator, recombinant nucleic acid, vector or host cell can be used for preparing a composition for preventing or treating CA 125 tumour antigen-associated disease in a mammal. The present sequence is used in the exemplification of the present invention.
CC	ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor sequences, and ACC44910 to ACC4493 encode the TSH receptor antibody VH and VL domains given in ABP96751 to ABP96778, which are used in the exemplification of the present invention.	CC	CC SQ Sequence 239 AA;
CC	Sequence 214 AA;	XX	XX Query Match 80.3%; Score 520.5; DB 6; Length 214;
CC	Best local similarity 80.0%; Pred. No. 2.6e-36; Matches 96; Conservative 13; Mismatches 10; Indels 1; Gaps 1;	XX	XX Query Match 80.0%; Score 518.5; DB 7; Length 239; Matches 96; Conservative 11; Mismatches 11; Indels 1; Gaps 1;
CC	Query 1 EIQLOQSGPSELVKVGASVYKSKAGSAGTNTYMMWYKOSHGSLEWVGYIDPYVGDGY 60	QY	1 EIQLOQSGPSELVKVGASVYKSKAGSAGTNTYMMWYKOSHGSLEWVGYIDPYVGDGY 60
CC	1 DVQHQGPSELVKVGASVYKSKAGSAGTNTYMMWYKOSHGSLEWVGYIDPYVGDGY 60	Db	1 QVQLOQSGPSELVKVGASVYKSKAGSAGTNTYMMWYKOSHGSLEWVGYIDPYVGDGY 60
CC	Query Match 80.3%; Score 520.5; DB 6; Length 214;	QY	61 SOKKGKATLIVDQSSAYMHNLTSRDAVYCARGNF PYFYDWGQSTLTWSS 119
CC	Best local similarity 80.0%; Pred. No. 2.6e-36; Matches 96; Conservative 13; Mismatches 10; Indels 1; Gaps 1;	Db	61 NOKFEGKATLIVDQSSAYMHNLTSRDAVYCARGNF PYFYDWGQSTLTWSS 118
CC	Query 1 EIQLOQSGPSELVKVGASVYKSKAGSAGTNTYMMWYKOSHGSLEWVGYIDPYVGDGY 60	RESULT 13	1 DVQHQGPSELVKVGASVYKSKAGSAGTNTYMMWYKOSHGSLEWVGYIDPYVGDGY 60
CC	Query Match 80.3%; Score 520.5; DB 6; Length 214;	ADC27445	ADC27445

ID ADC27445 standard; protein: 117 AA.
 XX
 AC ADC27445;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE TMERF2#20 heavy chain variable region SEQ ID NO:14.
 KW antibody; TMERF2#119; TMERF2; binding inhibitor; prostate cancer;
 KW cytostatic; vaccine; primary prostate cancer; metastatic prostate cancer;
 KW locally advanced prostate cancer; androgen independent prostate cancer;
 XX
 OS Synthetic.
 XX
 XX WO2003075855-A2.
 PN
 XX
 PD 18-SEP-2003.
 XX
 PP 07-MAR-2003; 2003WO-US007209.
 PR 08-MAR-2002; 2002US-0362837P.
 PR 27-DEC-2002; 2002US-0436812P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PT Bhaskar V, De La Calle A, Law D, Caras I, Ramakrishnan V;
 PI Murray R, Afar D, Powers D;
 XX
 PT WPI: 2003-756783/71.
 DR N-PSDB, ADC27444.
 XX
 PT New antibody that competitively inhibits binding of TMERF219 to TMERF2,
 PT useful for treating prostate cancer, e.g. primary, metastatic, locally
 advanced, or androgen independent prostate cancer.
 PT Example 1; SEQ ID NO 14; 51pp; English.
 XX
 CC The present invention describes an antibody (1) that competitively
 CC inhibits binding of TMERF2#19 to TMERF2. Also described: (1) a
 CC pharmaceutical composition comprising the antibody and a carrier; (2)
 CC detecting a prostate cancer cell in a biological sample from a patient by
 CC contacting the biological sample with the antibody; (3) inhibiting
 CC proliferation of a prostate cancer-associated cell by contacting the cell
 CC with the antibody; and (4) treating prostate cancer with an antibody to
 CC TMERF2. (1) has cytostatic activity and can be used in vaccines. The
 CC antibody, composition and method are useful for treating prostate cancer,
 CC e.g. primary prostate cancer, metastatic prostate cancer, locally
 CC advanced prostate cancer, androgen independent prostate cancer, prostate
 CC cancer that has been treated with neoadjuvant therapy, or prostate cancer
 CC that is refractory to treatment with neoadjuvant therapy. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ sequence 117 AA;

Query Match 79.8%; Score 517; DB 7; Length 117;
 Best Local Similarity 82.4%; Pred. No. 2, 8e-36;
 Matches 98; Conservative 9; Mismatches 10; Indels 2; Gaps 1;

QY 1 EIQHQSGSPELVKGASVSKVSKASGKAYARTNNMMWTKOSHKSLENGIDPYGDPY 60
 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 61 SOKERKGKATLTVDKSSSTAYMHNLTSEDSAVYCARGRGNF-PYFYDWGCGTTJWSS 117
 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 RESULT 14
 ABP96756 ID ABP96756 standard; protein: 214 AA.
 XX
 AC ABP96756;
 XX

DT 05-JUN-2003 (first entry)
 XX
 DE TSH receptor antibody 16E5 heavy chain amino acid sequence.
 XX
 KW Thyrotropin receptor; TSH receptor; epitope region; antibody;
 KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
 KW gene therapy; immune reaction; thyroid cancer.
 OS Synthetic.
 XX
 PN WO2003018632-A2.
 XX
 PD 06-MAR-2003.
 XX
 PR 21-AUG-2002; 2002WO-GB003931.
 XX
 PR 23-AUG-2001; 2001GB-0002049.
 PR 01-JUL-2002; 2002GB-00015212.
 XX
 PA (RSRR-) RSR LTD.
 XX
 PI Smith BR, Furmaniak J, Sanders JR;
 DR WPI: 2003-290551/28.
 DR N-PSDB; ACC44911.
 XX
 PT New polypeptide sequence having part or all of the primary structural
 PT conformation of one or more TSH receptor epitopes, useful for treating an
 PT autoimmune disease associated with an immune reaction to a TSH receptor,
 PT e.g. thyroid cancer.
 XX
 PS Claim 67; Fig 14; 196pp; English.
 XX
 CC The present invention describes a polypeptide sequence comprising part or
 CC all of the primary structural conformation of one or more thyrotropin
 CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
 CC produced in response to a TSH receptor interact. Also described: (1) one
 CC or more receptor TSH epitopes with which the autoantibodies and/or
 CC lymphocytes interact, as with the polypeptide sequence described above;
 CC (2) a method of screening for autoantibodies or lymphocytes produced in
 CC response to a TSH receptor in a sample of body fluid obtained from a
 CC subject suspected of suffering from, susceptible to, having or recovering
 CC from autoimmune disease associated with an immune reaction to a TSH
 CC receptor; (3) a binding partner for a TSH receptor, which is capable of
 CC binding to a TSH receptor to stimulate the TSH receptor, where the
 CC binding partner does not comprise TSH or naturally produced antibodies to
 CC the TSH receptor; and (4) a combination comprising the binding partner
 CC and one or more further agents capable of stimulating thyroid tissue,
 CC and/or tissue containing a TSH receptor, for simultaneous, separate or
 CC sequential use in stimulating thyroid tissue, and/or tissue containing a
 CC TSH receptor. A TSH receptor has cytostatic activity and can be used in
 CC gene therapy. The polypeptide, compositions and methods from the present
 CC invention can be used for treating an autoimmune disease associated with
 CC an immune reaction to a TSH receptor. The specific binding partner is
 CC useful for the manufacture of a medicament for stimulating thyroid tissue
 CC or tissue containing a TSH receptor, and for treating thyroid cancer.
 ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
 sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
 CC and VL domains given in ABP96751 to ABP96778, which are used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 214 AA;

Query Match 79.7%; Score 516.5; DB 6; length 214;
 Best Local Similarity 80.8%; Pred. No. 5.6e-36;
 Matches 97; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIQHQSGSPELVKGASVSKVSKASGKAYARTNNMMWTKOSHKSLENGIDPYGDPY 60
 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 61 SOKERKGKATLTVDKSSSTAYMHNLTSEDSAVYCARGRGNF-PYFYDWGCGTTJWSS 117
 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 QY 61 SOKERKGKATLTVDKSSSTAYMHNLTSEDSAVYCARGRGNF-PYFYDWGCGTTJWSS 119
 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 XX

Db 61 NQKFEDKATIVDVKSSSTAYMQLNSLTSEDSAVYCARRWWDWDPYAMDYWQGQGISVTVSS 120
 RESULT 15
 ABP6755 standard; protein; 214 AA.
 XX
 AC ABP6755;
 XX DT 05-JUN-2003 (first entry)
 XX DB TSH receptor antibody 15E5 heavy chain amino acid sequence.
 XX KW Thyrotropin receptor; TSH receptor; epitope region; antibody;
 KW autoantibody; autoimmune disease; thyroid tissue; Cytostatic;
 KW gene therapy; immune reaction; thyroid cancer.
 XX OS Synthetic.
 XX PN WO2003018632-A2.
 XX PD 06-MAR-2003.
 XX PR 21-AUG-2002; 2002WO-GB003831.
 XX PR 23-AUG-2001; 2001GB-00020649.
 PR 01-JUL-2002; 2002GB-00015212.
 XX PA (RSR-) RSR LTD.
 XX PT Smith BR, Furmaniak J, Sanders JP;
 DR XX WPI; 2003-29051/28.
 DR N-PSDB; ACC44910.
 XX PT New polypeptide sequence having part or all of the primary structural conformation of one or more TSH receptor epitopes, useful for treating an autoimmune disease associated with an immune reaction to a TSH receptor, e.g. thyroid cancer.
 XX PS Claim 71; Fig 13; 196pp; English.
 XX CC The present invention describes a polypeptide sequence comprising part or all of the primary structural conformation of one or more thyrotropin (TSH) receptor epitopes with which autoantibodies and/or lymphocytes produced in response to a TSH receptor interact. Also described: (1) one or more receptor TSH epitopes with which the autoantibodies and/or lymphocytes interact, as with the polypeptide sequence described above; (2) a method of screening for autoantibodies or lymphocytes produced in response to a TSH receptor in a sample of body fluid obtained from a subject suspected of suffering from, susceptible to, having or recovering from autoimmune disease associated with an immune reaction to a TSH receptor; (3) a binding partner for a TSH receptor, which is capable of binding to a TSH receptor to stimulate the TSH receptor, where the binding partner does not comprise TSH or naturally produced antibodies to the TSH receptor; and (4) a combination comprising the binding partner and one or more further agents capable of stimulating thyroid tissue, and/or tissue containing a TSH receptor, for simultaneous, separate or sequential use in stimulating thyroid tissue, and/or tissue containing a TSH receptor. A TSH receptor has cytoregulatory activity and can be used in gene therapy. The polypeptide, compositions and methods from the present invention can be used for treating an autoimmune disease associated with an immune reaction to a TSH receptor. The specific binding partner is useful for the manufacture of a medicament for stimulating thyroid tissue or tissue containing a TSH receptor, and for treating thyroid cancer. ACC44874 to ACC44905 and ABP6719 to ABP6750 represent TSH receptor sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH and VL domains given in ABP6751 to ABP6778, which are used in the exemplification of the present invention.
 XX SQ Sequence 214 AA;

Query Match 79.7%; Score 516.5; DB 6; Length 214;

THIS PAGE BLANK (uspto)

QY 1 BILOQSGPELVKGASVVKSCASGYAFTNMYWYKOSHGSLEWIGYIDPYGDPGY 60
 Db 1 EIQLOQSGAEVLVKGASVVKSCASGYAFTNMYWYKOSHGSLEWIGYIDPYGDPGY 60
 QY 61 SOKFKGATLTVDKSSTAYMHANSITSESDAVYKCA--RKGIPYIDWQGQTLT 116
 Db 61 NOKFKGATLTVDKSSTAYMHANSITSESDAVYKCA--RKGIPYIDWQGQTLT 116
 QY 117 VS 118
 Db 118 VS 119
 Db 118 VS 119

RESULT 3

I37267 Ig heavy chain V region (129) - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: I37267
 R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
 J. Biol. Chem. 266, 6607-6613, 1991
 A;Title: Heavy and light chain variable region sequences and antibody properties of anti
 A;Reference number: A38740; PMID:91177923; PMID:1706720
 A;Accession: I37267
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-128 <RUF>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;19-102/Domain: immunoglobulin homology <IMM>
 Query Match 78.3%; Score 507.5; DB 2; Length 128;
 Best Local Similarity 79.7%; Pred. No. 8.2e-38;
 Matches 98; Conservative 5; Mismatches 15; Indels 5; Gaps 1;
 QY 2 IOLQSGPELVKGASVVKSCASGYAFTNMYWYKOSHGSLEWIGYIDPYGDPGY 61
 Db 6 VOLQSGPELVKGASVVKSCASGYAFTNMYWYKOSHGSLEWIGYIDPYGDPGY 65
 QY 62 QKFKKATLTVDKSSTAYMHANSITSESDAVYCARHG---NFPTYPDWQGQTLT 116
 Db 66 QKFKKATLTVDKSSTAYMHANSITSESDAVYCARHG---NFPTYPDWQGQTLT 125
 QY 117 VSS 119
 Db 126 VSS 128

RESULT 4

C37267 Ig heavy chain V region (Py69) - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: C37267
 R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
 J. Biol. Chem. 266, 6607-6613, 1991
 A;Title: Heavy and light chain variable region sequences and antibody properties of anti
 A;Reference number: A38740; PMID:91177923; PMID:1706720
 A;Accession: C37267
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-128 <RUF>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 C;Keywords: heterotetramer; immunoglobulin
 F;19-102/Domain: immunoglobulin homology <IMM>
 Query Match 78.0%; Score 505.5; DB 2; Length 128;
 Best Local Similarity 78.0%; Pred. No. 1.2e-37;
 Matches 96; Conservative 7; Mismatches 15; Indels 5; Gaps 1;
 QY 2 IOLQSGPELVKGASVVKSCASGYAFTNMYWYKOSHGSLEWIGYIDPYGDPGY 61
 Db 6 VOLQSGPELVKGASVVKSCASGYAFTNMYWYKOSHGSLEWIGYIDPYGDPGY 61
 QY 62 QKFKKATLTVDKSSTAYMHANSITSESDAVYCARHG---NFPTYPDWQGQTLT 119

RESULT 5

A27609 Ig heavy chain precursor V region (I29) - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: A27609
 R;Klein, D.; Niecupski, J.; Shilin, S.; Stavnezer, J.
 J. Immunol. 140, 1675-1684, 1988
 A;Title: I-29 lymphoma cells express a nonmutated V-H gene before and after H chain swi.
 A;Reference number: A27609; PMID:88154467; PMID:3126234
 A;Accession: A27609
 A;Molecule type: DNA
 A;Residues: 1-129 <RUE>
 A;Cross-references: EMBL:M19401; NID:gi95441; PIDN:AAA38303.1; PID:9553992
 A;Genetics:
 A;Introns: 16/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-19/Domain: Signal sequence #status Predicted <SIG>
 F;20-139/Product: Ig heavy chain V region I29 #status Predicted <VAR>
 F;34-117/Domain: immunoglobulin homology
 Query Match 77.7%; Score 503.5; DB 2; Length 139;
 Best Local Similarity 80.0%; Pred. No. 2e-37;
 Matches 96; Conservative 10; Mismatches 13; Indels 1; Gaps 1;
 QY 1 BILOQSGPELVKGASVVKSCASGYAFTNMYWYKOSHGSLEWIGYIDPYGDPGY 60
 Db 20 EVOLQSGPELVKGASVVKSCASGYAFTDYMHWVKOSHGSLEWIGYINPYDTSY 79
 QY 61 SOKFKGATLTVDKSSTAYMHANSITSESDAVYCARHG---NFPTYPDWQGQTLT 119
 Db 80 NOKFKGATLTVDKSSTAYMHANSITSESDAVYCARHVSYSYAMDWQGQTLTVSS 139

RESULT 6

F37266 Ig heavy chain V region (Py2) - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: F37266
 R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
 J. Biol. Chem. 266, 6607-6613, 1991
 A;Title: Heavy and light chain variable region sequences and antibody properties of anti
 A;Reference number: A38740; PMID:91177923; PMID:1706720
 A;Accession: F37266
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-121 <RUF>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 C;Keywords: heterotetramer; immunoglobulin
 F;19-100/Domain: immunoglobulin homology <IMM>
 Query Match 77.0%; Score 499; DB 2; Length 121;
 Best Local Similarity 81.4%; Pred. No. 4.3e-37;
 Matches 96; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY 2 IOLQSGPELVKGASVVKSCASGYAFTNMYWYKOSHGSLEWIGYIDPYGDPGY 61
 Db 6 VOLQSGPELVKGASVVKSCASGYAFTNMYWYKOSHGSLEWIGYIDPYGDPGY 61
 QY 62 QKFKKATLTVDKSSTAYMHANSITSESDAVYCARHG---NFPTYPDWQGQTLTVSS 119

RESULT 7	Db	61 SQKEKGKATLTVDKSSTAYMELRSITSDDSAVYCAR--DYYFDWGAQTTIVSS 119
033305		Ig heavy chain V region (6B12) - mouse (fragment)
C;Species: Mus musculus (house mouse)		C;Species: Mus sp. (mouse)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999		C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C;Accession: JL0044; S05276; S03305		C;Accession: JL0044; S05276; T01407
R;Van Cleve, V.H.; Naeve, C.W.; Metzger, D.W.		R;Makashii, S.; Matsuura, Y.; Taniguchi, T.; Tamura, H.; Bitch, S.; Onishi, S.; Microbiol. Immunol. Med. 167, 1841-1848, 1988
A;Title: Do antibodies recognize amino acid side chains of protein antigens independent of antigenic determinants?		A;Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic determinants
A;Reference number: JL0043; MUID:88258372; PMID:2455014		A;Reference number: ZI4317; MUID:93116638; PMID:1474935
A;Accession: JL0044		A;Accession: T01407
A;Molecule type: mRNA		A;status: translated from GB/EMBL/DBJ
A;Residues: 1-117 <VAN>		A;Molecule type: mRNA
A;Cross-references: EMBL:X12381		A;Residues: 1-140 <TAK>
R;Metzger, D.W.		A;Cross-references: EMBL:S51851; PMID:9262657
submitted to the EMBL Data Library, July 1988		A;Superfamily: immunoglobulin V region; immunoglobulin homology
A;Reference number: S05276		Query Match 76.1%; Score 496; DB 2; Length 140;
A;Molecule type: mRNA		Best Local Similarity 79.8%; Pred. No. 1.7e-37;
A;Residues: 1-116 'T' <MET>		Mismatches 95; Conservative 9; Mismatches 13; Indels 2; Gaps 1;
A;Cross-references: EMBL:X12381; NID:952094; PIDN:CAA30939.1; PID:9930170		Db
C;Superfamily: immunoglobulin V region; immunoglobulin homology		Qy 1 BIOLQQSGLPELVKGASVKUSCKASGYATNNMMWVKOSHGSLEMIQYDYYGDCEY 60
C;Keywords: heterotetramer; immunoglobulin		Db 1 EVQLQOSGPBEGKKGAVSNCKSKASGYTETDYINWVKOSHGSLEWIGYIENDEPAY 60
F;15-98/Domain: immunoglobulin homology <IMM>		Qy 61 SQKEKGKATLTVDKSSTAYMELRSITSDDSAVYCAR--DYYFDWGAQTTIVSS 119
Query Match 76.5%; Score 496; DB 2; Length 117;		Db 61 SQKEKGKATLTVDKSSTAYMELRSITSDDSAVYCAR--DYYFDWGAQTTIVSS 119
Best Local Similarity 80.7%; Pred. No. 7.7e-37;		Qy 80 NOKFRKGKATLTVDKSSTAYMQLNSLTSDDSAVYCAR--DYYFDWGAQTTIVSS 136
Mismatches 96; Conservative 6; Mismatches 15; Indels 2; Gaps 1;		Db
RESULT 8		Qy 1 BIOLQQSGLPELVKGASVKUSCKASGYATNNMMWVKOSHGSLEMIQYDYYGDCEY 60
MMS4B		Db 20 EVQLQOSGPBEGKKGAVSNCKSKASGYTETDYINWVKOSHGSLEWIGYIENDEPAY 79
Ig heavy chain V region (MOPC 104E) - mouse (tentative sequence)		Qy 61 SQKEKGKATLTVDKSSTAYMELRSITSDDSAVYCAR--DYYFDWGAQTTIVSS 119
C;Species: Mus musculus (house mouse)		Db 80 NOKFRKGKATLTVDKSSTAYMQLNSLTSDDSAVYCAR--DYYFDWGAQTTIVSS 136
C;Date: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004		Qy 1 BIOLQQSGLPELVKGASVKUSCKASGYATNNMMWVKOSHGSLEMIQYDYYGDCEY 60
C;Accession: A02039		Db 20 EVQLQOSGPBEGKKGAVSNCKSKASGYTETDYINWVKOSHGSLEWIGYIENDEPAY 79
R;Henry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.		Qy 61 SQKEKGKATLTVDKSSTAYMELRSITSDDSAVYCAR--DYYFDWGAQTTIVSS 119
Biochemistry 21, 5415-5424, 1982		Db 80 NOKFRKGKATLTVDKSSTAYMQLNSLTSDDSAVYCAR--DYYFDWGAQTTIVSS 136
A;Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain components		Qy 1 BIOLQQSGLPELVKGASVKUSCKASGYATNNMMWVKOSHGSLEMIQYDYYGDCEY 60
A;Reference number: A02039; MUID:83075344; PMID:6816276		Db 20 EVQLQOSGPBEGKKGAVSNCKSKASGYTETDYINWVKOSHGSLEWIGYIENDEPAY 79
A;Molecule type: protein		Qy 61 SQKEKGKATLTVDKSSTAYMELRSITSDDSAVYCAR--DYYFDWGAQTTIVSS 119
A;Residues: 1-117 <KEH>		Db 80 NOKFRKGKATLTVDKSSTAYMQLNSLTSDDSAVYCAR--DYYFDWGAQTTIVSS 136
A;Cross-references: UNIPROT:P01756		Qy 1 BIOLQQSGLPELVKGASVKUSCKASGYATNNMMWVKOSHGSLEMIQYDYYGDCEY 60
C;Comment: The glycosylated asparagine residue does not have the usual N-X-S/T context at position 117.		Db 5 EVQLQOSGPBEGKKGAVSNCKSKASGYTETDYINWVKOSHGSLEWIGYIENDEPAY 64
C;Superfamily: immunoglobulin V region; immunoglobulin homology		Qy 61 SQKEKGKATLTVDKSSTAYMELRSITSDDSAVYCAR--DYYFDWGAQTTIVSS 119
C;Keywords: glycoprotein; heterotetramer; immunoglobulin		Db 65 NORFKGKATLTVDKSSTAYMELRSITSDDSAVYCAR--DYYFDWGAQTTIVSS 124
F;15-98/Domain: immunoglobulin homology <IMM>		Qy 116 TVSS 119
F;22-96/Disulfide bonds: #status predicted		Db 125 TVSS 128
P;55/Binding site: carbohydrate (Asn) (covalent) #status atypical		
Query Match 76.1%; Score 493; DB 1; Length 117;		
Best Local Similarity 79.8%; Pred. No. 1.4e-36;		
Matches 95; Conservative 9; Mismatches 13; Indels 2; Gaps 1;		
RESULT 9		
T01407		
Ig heavy chain (myeloma M104E) - mouse (fragment)		
C;Species: Mus sp. (mouse)		
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000		
C;Accession: T01407		
R;Makashii, S.; Matsuura, Y.; Taniguchi, T.; Tamura, H.; Bitch, S.; Onishi, S.; Microbiol. Immunol. Med. 167, 1841-1848, 1988		
A;Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic determinants		
A;Reference number: ZI4317; MUID:93116638; PMID:1474935		
A;Accession: T01407		
A;status: translated from GB/EMBL/DBJ		
A;Molecule type: mRNA		
A;Residues: 1-140 <TAK>		
A;Cross-references: EMBL:S51851; PMID:9262657		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the EMBL Data Library, July 1988		
A;Reference number: S05276		
A;Molecule type: mRNA		
A;Residues: 1-117 <VAN>		
A;Cross-references: EMBL:X12381		
R;Metzger, D.W.		
submitted to the E		

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C;Accession: Pn0444
 R;Kiluza, B.; Betz, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
 Gene 122, 321-328, 1992
 A;Title: A general method for chimerization of monoclonal antibodies by inverse polymerase
 A;Reference number: Pn044; MUID:93138402; PMID:1339379
 A;Accession: Pn0444
 A;Molecule type: mRNA
 A;Residues: 1-150 <RUR>
 A;Cross-references: GB:102346
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-19/Domain: signal sequence #status Predicted <SIG>
 F;20-150/Domain: Ig heavy chain V region #status predicted <MAT>
 F;20-117/Domain: variable region <VRG>
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.7%; Score 490.5; DB 2; Length 150;
 Best Local Similarity 78.2%; Pred. No. 3e-36; Matches 93; Conservative 9; Mismatches 16; Indels 1; Gaps 1; Matches 93; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

Qy 1 BILOQSGPVELVKPGASVYKVSCKASGYAFINTNMYWIKOSHGSLEWIGIDPYGDPGY 60
 Db 20 EVOLQSGPVELVKPGASVYKVSCKASGYITDYNNDWIKQSHGSLEWIGIDPYGDPGY 79

Qy 61 SQEKKGKATLTVDKSSSTAYMHSNLTSEDSAVYCARRGNFPPYFDWGGQFTLTIVS 119
 Db 80 NQKFKGKATLTVDKSSNTAMELSLTSEDTAVYCA RGQPPGMDFWGQTSVTSS 137

RESULT 12
 MHMSJ5
 Ig heavy chain V region (J558) - mouse (tentative sequence)
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C;Accession: M26242
 R;Schilling, J.; Clevinger, B.; Davie, J.M.; Hood, L.
 Nature 283, 35-40, 1980
 A;Title: Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements
 A;Reference number: A26242; MUID:80078170; PMID:6765983
 A;Accession: A26242
 A;Molecule type: protein
 A;Residues: 1-117 <SCH>
 A;Cross-references: UNIPROT:P01757
 A;Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that in
 C;Comment: This protein binds dextran.
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; hybridoma; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>
 F;22-96/Disulfide bonds: #status predicted

Query Match 74.8%; Score 485; DB 1; Length 117;
 Best Local Similarity 79.8%; Pred. No. 7.1e-35; Matches 95; Conservative 8; Mismatches 14; Indels 2; Gaps 1; Gaps 1; Matches 95; Conservative 8; Mismatches 14; Indels 2; Gaps 1;

Qy 1 EIQOQSGPVELVKPGASVYKVSCKASGYAFINTNMYWIKOSHGSLEWIGIDPYGDPGY 60
 Db 1 EVOLQSGPVELVKPGASVYKVSCKASGYITDYNNDWIKQSHGSLEWIGIDPYGDPGY 60

Qy 61 SQEKKGKATLTVDKSSSTAYMHSNLTSEDSAVYCARRGNFPPYFDWGGQFTLTIVS 119
 Db 61 NQKFKGKATLTVDKSSNTAMELSLTSEDTAVYCA RGQPPGMDFWGQTSVTSS 137

RESULT 13
 H37266
 Ig heavy chain V region (P54) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
 C;Accession: H37266
 R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Gleimeney Jr., J.R.
 J. Biol. Chem. 266, 6607-6613, 1991
 A;Title: Heavy and light chain variable region sequences and antibody properties of anti-

A;Reference number: A38740; MUID:9117793; PMID:1706720
 A;Accession: H37266
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-121 <RUR>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;19-100/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 483; DB 2; Length 121;
 Best Local Similarity 79.7%; Pred. No. 1.1e-35; Matches 94; Conservative 8; Mismatches 14; Indels 2; Gaps 1; Matches 94; Conservative 8; Mismatches 14; Indels 2; Gaps 1;

Qy 2 ILOQSGPVELVKPGASVYKVSCKASGYAFINTNMYWIKOSHGSLEWIGIDPYGDPGY 61
 Db 6 VOLQSGPVELVKPGASVYKVSCKASGYITDYNNDWIKQSHGSLEWIGIDPYGDPGY 63

Qy 62 QKEKGKATLTVDKSSSTAYMHSNLTSEDSAVYCARRGNFPPYFDWGGQFTLTIVS 119
 Db 64 QKFRKGKATLTVDKSSSTAYMERSNLTSEDSAVYCARGDNLVYFDWGGQFTLTIVS 121

RESULT 14
 PL0200
 anti-DNA autoantibody BV16-19, heavy chain V region - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: PL0200
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 R;Smith, R.G.; Voss Jr., E.W.
 Mol. Immunol. 27, 463-470, 1990
 A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from
 A;Reference number: PL0198; MUID:90309768; PMID:2114528
 A;Accession: PL0200
 A;Molecule type: mRNA
 A;Residues: 1-18 <SMI>
 A;Cross-references: GB:X33641; MUID:950193; PID:9930139
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;15-98/Domain: immunoglobulin homology <IMM>
 F;31-35/Region: complementarity-determining 1
 F;50-66/Region: complementarity-determining 2
 F;99-110/Region: complementarity-determining 3
 F;99-106/Region: D region
 F;107-118/Region: JH region

Query Match 74.2%; Score 481; DB 2; Length 118;
 Best Local Similarity 78.8%; Pred. No. 1.6e-35; Matches 93; Conservative 8; Mismatches 15; Indels 2; Gaps 1; Gaps 1; Matches 93; Conservative 8; Mismatches 15; Indels 2; Gaps 1;

Qy 1 EIQOQSGPVELVKPGASVYKVSCKASGYAFINTNMYWIKOSHGSLEWIGIDPYGDPGY 60
 Db 1 BILOQSGPVELVKPGASVYKVSCKASGYITDYNNDWIKQSHGSLEWIGIDPYGDPGY 60

Qy 61 SQEKKGKATLTVDKSSSTAYMHSNLTSEDSAVYCARRGNFPPYFDWGGQFTLTIVS 116
 Db 61 NQKFKGKATLTVDKSSNTAMELSLTSEDTAVYCA RGQPPGMDFWGQTSVTSS 118

RESULT 15
 PH0887
 Ig heavy chain V region (anti-CD3) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
 C;Accession: PH0887
 C;Molecule type: mRNA
 A;Residues: 1-122 <SMA>
 A;Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocytes
 A;Reference number: PH0885; MUID:92113462; PMID:1346155
 A;Accession: PH0887
 A;Molecule type: mRNA
 A;Residues: 1-122 <SMA>
 A;Title: The authors translated the codon RTC for residue 70 as Leu
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

P;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.5%; Score 476.5; DB 2; Length 122;

Best Local Similarity 74.6%; Pred. No. 4.1e-35; Matches 91; Conservative 11; Mismatches 17; Indels 3; Gaps 1;

Qy 1 EIQLOQSGPRLVKRGASVVKISKASGYAFTINNMWVKOSHGSLEWIGYIDPYGDPQY 60
Db 1 EIQLOQSGPRLVKRGASVVKISKASGYAFTINNMWVKOSHGSLEWIGYIDPYGDPQY 60

Qy 61 SQKPKGKATITVDKSSTAYNHNLNSLTSENSEAVVYCARRGNF---PYYFDYWGOOTTIV 117
Db 61 NQKFKDAKTTTVDKSSSTAMELSLTSITSEDSAVIYCARSQYYGDSDWIFDVWGAHTIV 120

Qy 118 SS 119
Db 121 SS 122

Search completed: December 29, 2004, 18:06:55
Job time : 17.4897 secs

THIS PAGE BLANK (USPS)

GenCore version 5.1.6									
OM protein - protein search, using sw model									
Run on: December 29, 2004, 17:38:43 ; Search time 82.1416 Seconds									
Scoring table: BLOSSUM62	Score: 1825181 seqs, 575374646 residues	Sequence: Gapop 10.0 , Gapext 0.5	Perfect score: 648	Title: US-10-774-076-2	Post-processing: Minimum Match 0%	Minimum DB seq length: 0	Maximum DB seq length: 200000000	Post-processing: Maximum Match 100%	Total number of hits satisfying chosen parameters: 1825181
Result No.	Score	Query Match Length	DB ID	Description	Result 1	Result 2	Result 3	Result 4	Result 5
1	509	78.5	117	Q9QXF0	Q9QXF0	Q9QXF0	Q9QXF0	Q9QXF0	Q9QXF0
2	501	77.3	470	07TMK1	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
3	500	77.2	120	0920EB	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
4	499	77.0	472	06PJA7	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
5	499	77.0	472	AHH18535	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
6	493	76.1	117	RV12_MOUSE	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
7	491	75.8	123	08VJU1	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
8	489.5	75.5	481	08VCV5	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
9	485	74.8	117	1T3X_MOUSE	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
10	485	74.8	117	09QXE9	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
11	469.5	72.5	488	09IWR1	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
12	463.5	71.5	118	HV07_MOUSE	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
13	462	71.3	146	0924R8	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
14	454	70.1	170	0925S2	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
15	452	69.8	136	HV15_MOUSE	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
16	450.5	69.5	139	1T3X_MOUSE	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
17	450.5	69.5	145	0924Q7	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
18	450	69.4	117	HV14_MOUSE	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
19	447.5	69.1	465	06FJB2	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
20	447.5	69.1	465	AAH18200	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
21	444	69.1	488	08K0F2	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
22	444	69.1	120	1T3X_MOUSE	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
23	444	68.5	144	0924P5	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
24	440.5	68.0	145	0924R8	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
25	439.5	67.8	109	09JL75	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
26	439.5	67.8	137	0924R6	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
27	438.5	67.7	145	0924R6	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
28	438.5	67.7	2	0924R1	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
29	438	67.6	142	0924Q1	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
30	438	67.6	2	091W1	09qxf0	09qxf0	09qxf0	09qxf0	09qxf0
31	437.5	67.5	143	2	0924R7	09qxf0	09qxf0	09qxf0	09qxf0

			[1]
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CZECH II;		
RN	TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.		
RC	Expression driven by an MMTV-LTR enhancer.;		
RX	MEDLINE=22388257; PubMed=12479932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klaushner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,		
RA	Diatchenko L., Marsina K., Farmer A.M., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquett-Llano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Krzywinski M.I., Skalska U., Smilis D.E., Schmerch A., Schein J.E.,		
RC	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.",		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RR	[2]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=CZECH II;		
RC	TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.		
RC	Expression driven by an MMTV-LTR enhancer.;		
RA	Strausberg R.;		
RA	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: BC05910; ARH5910.1; -.		
DR	InterPro: IPR007110; Ig-like.		
DR	InterPro: IPR030397; Ig_C1.		
DR	InterPro: IPR030306; Ig_MHC.		
DR	InterPro: IPR030396; Ig_V.		
PFAM	PF007654; Cl-set_3.		
DR	Pfam; PF00047; Ig_1.		
DR	SMART; SM00406; IgV_1.		
DR	PROSITE; PS50815; IG_LIKE_4.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.		
KW	Hypothetical protein.		
SEQUENCE	470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;		
Query Match	77.2%; Score 500; DB 2; Length 120;		
Matches	96; Conservative 7; Mismatched 15; Indels 2; Gaps		
OY	1 EIQOLQSGPELVKPGASKVSKCASKASGTYAFNTNMVKQKGKSLWIGLYIDPYGDPY 60		
Db	1 EVQLOSGSGPELVKPGASKVSKCASKASGTYAFNTNMVKQKGKSLWIGLYIDPYGDPY 61		
OY	61 SQKFHKSKATLTDKSSTAYHHLNSITSEDAVYKAR--RGNFPPYYFDWQGQTTLTV 1		
Db	61 NQKFHKSKATLTDKSSTAYHHLNSITSEDAVYKAR--RGNFPPYYFDWQGQTTLTV 11		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Czech II;		
RC	TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.		
RC	Expression driven by an MMTV-LTR enhancer.;		
RX	MEDLINE=22388257; PubMed=12479932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klaushner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.P., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,		
RA	Diatchenko L., Marsina K., Farmer A.M., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquett-Llano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Krzywinski M.I., Skalska U., Smilis D.E., Schmerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.",		
DT	01-DEC-2001 (TREMBLrel. 19, created)		
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)		
DE	Pterin-mimicking anti-idiotope heavy chain variable region (Fragment).		
DE	Mus musculus (Mouse).		
RESULT	3		
Q9205B	PRELIMINARY; PRT; 120 AA.		
Q9205B	09205B; 01-DEC-2001 (TREMBLrel. 19, created)		
Q9205B	01-OCT-2003 (TREMBLrel. 25, last annotation update)		
Q9205B	Pterin-mimicking anti-idiotope heavy chain variable region (Fragment).		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=Czech II;		
RC	TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.		
RC	Expression driven by an MMTV-LTR enhancer.;		
RX	MEDLINE=22388257; PubMed=12479932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klaushner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.P., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,		
RA	Diatchenko L., Marsina K., Farmer A.M., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquett-Llano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Krzywinski M.I., Skalska U., Smilis D.E., Schmerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.",		
DT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Czech II;		
RC	TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.		

RC Expression driven by an MMTV-LTR enhancer.;

RA Strausberg R.,

RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC018535; AAIH18535.1; -.

DR InterPro; IPR03599; Ig-like.

DR InterPro; IPR03597; Ig-cl.

DR InterPro; IPR03006; Ig_MHC.

DR InterPro; IPR03595; Ig_v.

DR Pfam; PF07654; C1-set; 3.

DR SMART; SM00407; Ig_4.

DR SMART; SM00406; Ig_v.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 472 AA; 52299 MW; 165169C23D55D4AB CRC64;

Query Match 77.0%; Score 499; DB 2; Length 472;

Best Local Similarity 78.0%; Pred. No. 3.1e-41;

Matches 96; Conservative 10; Mismatches 13; Indels 4; Gaps 1;

QY 1 BILOQOSGPBLVKPGASVRSKASGTYAFTNNMWTQSHGKSLWIGYIDPYGDCY 60

Db 20 EVOLQSGPBLVKPGASVRSKASGTYAFTNNMWTQSHGKSLWIGYIDPYGDCY 79

QY 61 SOKERKGKATITVDKSSTAYMHNLISLTSBESAVYCAR---RGNPPYFDYNGQGTT 116

Db 80 :|||||SOKERKGKATITVDKSSTAYMHNLISLTSBESAVYCAR---RGNPPYFDYNGQGTT 139

QY 117 VSS 119

Db 140 VSS 142

RESULT 5

ARH18535 PRELIMINARY; PRT; 472 AA.

AC AAIH18535;

DT 02-MAR-2004 (TREMBREL. 27, Created)

DT 02-MAR-2004 (TREMBREL. 27, Last annotation update)

DT 02-MAR-2004 (TREMBREL. 27, Last annotation update)

DB Hypothetical protein.

OS Mus musculus (Mouse).

OC Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Czech II; TISSUE=Mammary tumor;

RX MEDLINE=22389257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RX Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,

RA Altschul S.P., Zeeberg B., Butow K.H., Schaefer C.F., Bhattacharyya N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,

RA Blatchko L., Mansura K., Farmer A.A., Robin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Ratai S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

RA Bosak S.A., McEwan P.J., McFernan K.J., Malek J.A., Gunnarane P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green R.D., Dickson M.C.,

RA Rodriguez A.C., Grifwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalius D.E., Schnurch A., Schein J.E.,

RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=Czech II; TISSUE=Mammary tumor;

RA Strausberg R.,

RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC018535; AAIH18535.1; -.

DR InterPro; IPR03599; Ig-like.

DR InterPro; IPR03597; Ig-cl.

DR InterPro; IPR03006; Ig_v.

DR PROSITE; PS00835; Ig_Like; 1.

DR direct protein sequencing; Glycoprotein; Immunoglobulin V region.

FT DOMAIN 1 116 Ig-like.

FT DISUFRID 22 96 BY similarity.

FT CARBOHYD 55 55 N-linked (GlyNAc. . .) (complex).

FT NON_TER 117 117

FT SEQUENCE 117 AA; 12983 MW; 3CP8ACE4BE447B41 CRC64;

Query Match 76.1%; Score 493; DB 1; Length 117;

Best Local Similarity 79.8%; Pred. No. 2.4e-41;

Matches 95; Conservative 9; Mismatches 13; Indels 2; Gaps 1;

QY 1 BILOQOSGPBLVKPGASVRSKASGTYAFTNNMWTQSHGKSLWIGYIDPYGDCY 60

Db 1 EVOLQSGPBLVKPGASVRSKASGTYAFTNNMWTQSHGKSLWIGYIDPYGDCY 79

QY 61 SOKERKGKATITVDKSSTAYMHNLISLTSBESAVYCAR---RGNPPYFDYNGQGTT 116

Db 61 NOKFKGKATLTVDKSSSTAYMOLNLSITSEDSAVYCCAR--DYDWFDFWAGTTVVSS 117
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Caninici P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Borak S.A., McEwan P.J., McKerman K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smilus D.E., Schneirach A., Schein J.E.,
RA Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]

RN [1] SEQUENCE FROM N.A.
RP STRAIN=C3H/HeJ-1Pr./1Pr/
RX MEDLINE=98409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-1Pr mice and lupus mice with nephritis."
RL Bur. J. Immunol. 222:22-23 (1996).
DR EMBL: U59154; AAB02916.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003595; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00405; IgV_1.
DR PROSITE; PS50335; Ig_LIKE; 1.
FT NON_TER 1
FT NON_TER 123
FT SEQUENCE 123 AA; 123 MW; CCO037A806E9911E CRC64;

Query Match 75.8%; Score 491; DB 2; Length 123;
Best Local Similarity 76.8%; Pred. No. 4.1e-41;
Matches 96; **Conservative** 8; **Mismatches** 13; **Indels** 8; **Gaps** 2;

QY 1 BILOQSGPVLVKPGASVKRICKSAGYAFNTNNMVKWKGSHGKSLIEWIGYIDPYVGGY 60
DB 1 EIQLOQSGPVLVKPGASVKRICKSAGYAFNTNNMVKWKGSHGKSLIEWIGYIDPYVGGY 60
QY 61 SOKFKGKATLTVDKSSSTAYMOLNLSITSEDSAVYCCAR--DYDWFDFWAGTTVVSS 117
DB 61 SOKFKGKATLTVDKSSSTAYMOLNLSITSEDSAVYCCAR--DYDWFDFWAGTTVVSS 118
QY 115 LTVSS 119
DB 119 :||:
DB 119 VTUSA 123

RESULT 8

Q8VCV5 PRELIMINARY; PRT; 481 AA.

AC Q8VCV5;
DT 01-MAR-2002 (Trembleur. 20, Created)
DT 01-MAR-2002 (Trembleur. 20, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=mix FVB/N;
RA Tissue-Mammary tumor. WAP-TGF alpha model. 7 months old;
RA MEDLINE=2288257; PubMed=1247792;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.N., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heich P.,
RA Diatchenko L., Manuska K., Farmer A.A., Rubin G.M., Hong L.,

RESULT 9

HV13_MOUSE STANDARD; PRT; 117 AA.

AC HV13_MOUSE
DT 201757; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DB Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] SEQUENCE.
RP MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Cleveringer B., Davie J.M., Hood L.,
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT reactivities in heavy chain V-region gene segments";
RL Nature 203:35-40 (1980).
CC -!- MISCELLANEOUS: The sequences of 10 hybrida proteins that also
CC bind dextran differ from that shown at the D and J positions, many of
CC which occur in the D and J segments.
CC -!- MISCELLANEOUS: This protein binds dextran.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A26242; MEMSUS.

DR HSSP; P01751; INQB. Igh-VJ558 protein.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003595; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50335; Ig_LIKE; 1.
 DR Direct protein sequencing; Immunoglobulin V region.
 KW DOMAIN; 1; 116
 PT DISTFLD; 22; 96
 PT NON_TER; 117; 117
 SQ SEQUENCE; 117 AA; 13024 MW; 292E2AFBEB47B41 CRC64;
 Query Match 74.8%; Score 485; DB 1; Length 117;
 Best local Similarity 79.8%; Pred. No. 1.5e-40;
 Matches 95; Conservative 8; Mismatches 14; Indels 2; Gaps 1;
 PT By similarity.

RESULT 10
 Q9QE9 PRELIMINARY; PRT; 117 AA.
 ID Q9QE9 PRELIMINARY; PRT; 117 AA.
 AC Q9QE9; 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DB Immunoglobulin heavy chain V-D-J region (Fragment).
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clemens A., Rademakers A., Specht C., Koelsch E.; Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RL EMBL; Au225174; CAB65237; 1; -.
 DR PIR; P33932; F33932.
 DR HSSP; P01751; INQB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 DR PROSITE; PS50835; Ig_v; 1.
 PT NON_TER; 1; 1
 FT SEQUENCE; 117 AA; 13000 MW; CDDE2AFB84D499734 CRC64;
 SQ Sequence 117 AA; 13000 MW; CDDE2AFB84D499734 CRC64;
 Query Match 74.8%; Score 485; DB 2; Length 117;
 Best local Similarity 79.8%; Pred. No. 1.5e-40;
 Matches 95; Conservative 8; Mismatches 14; Indels 2; Gaps 1;

Query Match 72.5%; Score 469.5; DB 2; Length 488;
 Best local Similarity 73.4%; Pred. No. 2.8e-38;
 Matches 91; Conservative 11; Mismatches 17; Indels 5; Gaps 1;

RESULT 11
 Q91WR1 PRELIMINARY; PRT; 488 AA.
 ID Q91WR1; 01-DEC-2001 (Tremblrel. 19, Created)
 AC Q91WR1; 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

RESULT 12
 HV51_MOUSE STANDARD; PRT; 118 AA.
 ID HV51_MOUSE
 AC P06330; 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DR DE Ig heavy chain V region AAC38 205.12.
 OS OC Mus musculus (Mouse)
 OC OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1] RN
 RP SSEQUENCE.
 RX MEDLINE=84182519; PubMed=6301362;
 DR Dildor R.; Bovens J.; Sickovitz M.; Beyreuther K.; Rajewsky K.;
 RT "A V region determinant (idiotope) expressed at high frequency in B
 RT lymphocytes is encoded by a large set of antibody structural genes.";
 RL EMBO J. 3:17-23(1984).
 DR PIR; A02040; MIM38.
 DR HSSP; P01731; INQB.
 DR InterPro; IPR0110; Ig-like.
 DR InterPro; IPR03596; Ig_v.
 DR Pfam; PF0047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 DR Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 98 V segment.
 FT DOMAIN 9 104 D segment.
 FT DOMAIN 105 118 J segment.
 FT DISULFID 22 96 By similarity.
 FT NON TER 118 118
 SQ SEQUENCE 118 AA; 12934 MW; 94F7BB4C762A108 CRC64;
 Query Match 71.5%; Score 463.5; DB 1; Length 118;
 Best Local Similarity 77.5%; Pred. No. 2.2e-38; Matches 93; Conservative 6; Mismatches 18; Indels 3; Gaps 2;
 QY 1 BIQLOQSGPELVIKPGASVURVKASGAFNTNMYWQSHRSKLSIGVYDPYDGPY 60
 1 EVQLQSGPELVIKPGASVURVKASGAFNTNMYWQSHRSKLSIGVYDPYDGPY 60
 61 SOKPKKGKALTVDKSSSTAYMHLNSLTSEDSAVYCAR-RGNPPYYDYGDTWSS 119
 61 NOKPKKGKALTVDKSSSTAYMHLNSLTSEDSAVYCAR-RGNPPYYDYGDTWSS 118
 Db 119 S 119
 Db 121 S 121
 RESULT 13
 ID Q924RB PRELIMINARY; PRT; 146 AA.
 AC Q924B8; 19, Created
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, last annotation update)
 DT VH185.2-D-J-C mu protein (Fragment).
 GN Name=VH185.2-D-J-C mu;
 OS Mus musculus (Mouse);
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1] RN
 RP SSEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB067781; BAB3266_1; -.
 PIR; F28833.
 PIR; PH1105; PH1105.
 PIR; PH1108; PH1108.
 PIR; PH1114; PH1114.
 PIR; PH1118; PH1118.
 PIR; PH1119; PH1119.
 PIR; PH1125; PH1125.
 PIR; PH1126; PH1126.
 PIR; PH1128; PH1128.
 PIR; PH1129; PH1129.
 PIR; PH1131; PH1131.
 PIR; PH1134; PH1134.
 PIR; PH1137; PH1137.
 PIR; PH1139; PH1139.

RESULT 14
 ID Q925S2 PRELIMINARY; PRT; 170 AA.
 AC Q925S2; 19, Created
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, last annotation update)
 DE MRPA.
 OS Mus musculus (Mouse);
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1] RN
 RP SSEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX PubMed=11819679;
 RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
 RA Su C.;
 RT "Mechanism of exogenous nucleic acids and their precursors improving
 RT the repair of intestinal epithelium after irradiation in mice.";
 RL World J. Gastroenterol. 6:709-717(2000).
 RN [2]
 RP SSEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Gui D., Zeng G., Yan X., Li X., Su C.;
 RT "Cloning of mouse genes related to repairing of intestinal epithelium
 RT of the irradiated mice by treatment with the intestinal RNA of mice of
 RT the same strain.";
 RL Inn. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80 (2001).
 DR EMBL; AF240167; AAK3732_1; -.
 DR HSSP; P01731; IAGW.
 DR InterPro; IPR00710; Ig-like.
 DR PIR; PH1152; PH1152.
 DR PIR; PH1153; PH1153.
 DR InterPro; IPR00710; Ig-like.
 DR InterPro; IPR03596; Ig_v.
 DR Pfam; PF0047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 DR SSEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match 70.1%; Score 454; DB 2; Length 170;

Best Local Similarity 68.0%; Pred. No. 2.9e-37;
 Matches 83; Conservative 19; Mismatches 16; Indels 4; Gaps 2;

Qy

1 BIQKQSGELVKPGASVVKRCKSGAFTNNYVWKQSHGSKLEWIGYIDPYGGY 60

Db

3 QVKLQSGEPVVRPGVSVKICKSGSYTDDYHMLKONHASSLEMGIISYDGNTW 62

Qy

61 SQKEFKGKATITVDKSSSTAYMHNLNSLTDSDAVYCAR--RGNPPYYDYMCGTTIV 117

Db

63 NOKEFKGKATITVDKSSITAYMELARLTSDDSAIYCARGYVGSF-YFDYWGQTTIV 121

Qy

118 SS 119

Db

122 SS 123

RESULT 15

HV15_MOUSE STANDARD; PRT; 136 AA.

ID

HV15_MOUSE P01759; 21-JUL-1986 (Rel. 01, Created)

DT

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB

DB Ig heavy chain V region BCL1 precursor.

OS

OS Mus musculus (Mouse).

OC

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC

OC Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC

OC NCBI_TaxId=10990; [1]

RN

RN MEDLINE-#2222262; PubMed=6806821;

RP

RP Krapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,

RA

RA Blattner F.R.;

RT

RT "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared by two adjacent CH genes.";

RT

RT Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).

CC

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

Search completed: December 29, 2004, 18:05:16
 Job time : 83.1416 secs

Query Match 69.8%; Score 452; DB 1; Length 136;
 Best Local Similarity 72.5%; Pred. No. 3.6e-37;
 Matches 87; Conservative 11; Mismatches 18; Indels 4; Gaps 2;
 Matches 87; Conservative 11; Mismatches 18; Indels 4; Gaps 2;

1 EIQLOQSGEPVELVKPGASVVKRCKSGAFTNNYVWKQSHGSKLEWIGYIDPYGGY 60
 20 QVOLQSGEPVVRPGVSVKICKSGSYTDDYHMLKONHASSLEMGIISYDGNTW 79

Qy 61 SQKEFKGKATITVDKSSSTAYMHNLNSLTDSDAVYCAR--RGNPPYYDYMCGTTIV 119
 80 NQKEFKGKATITVDKSSSTAYMHNLNSLTDSDAVYCAR--RGNPPYYDYMCGTTIV 119

THIS PAGE BLANK (USPTO)